```
                                       M   K   L   Q   C   V   S   L   W     9
GAATTCCGACAAGGAGCAGCCCGCAAGCACCAAGTGAGAGGC ATG AAG TTA CAG TGT GTT TCC CTT TGG    69

 L   L   G   T   I   L   I   L   C   S   V   D   N   H   G   L   R   R   C   L    29
CTC CTG GGT ACA ATA CTG ATA TTG TGC TCA GTA GAC AAC CAC GGT CTC AGG AGA TGT CTG  129

 I   S   T   D   M   H   H   I   E   E   S   F   Q   E   I   K   R   A   I   Q    49
ATT TCC ACA GAC ATG CAC CAT ATA GAA GAG AGT TTC CAA GAA ATC AAA AGA GCC ATC CAA  189

 A   K   D   T   F   P   N   V   T   I   L   S   T   L   E   T   L   Q   I   I    69
GCT AAG GAC ACC TTC CCA AAT GTC ACT ATC CTG TCC ACA TTG GAG ACT CTG CAG ATC ATT  249

 K   P   L   D   V   C   C   V   T   K   N   L   L   A   F   Y   V   D   R   V    89
AAG CCC TTA GAT GTG TGC TGC GTG ACC AAG AAC CTC CTG GCG TTC TAC GTG GAC AGG GTG  309

 F   K   D   H   Q   E   P   N   P   K   I   L   R   K   I   S   S   I   A   N   109
TTC AAG GAT CAT CAG GAG CCA AAC CCC AAA ATC TTG AGA AAA ATC AGC AGC ATT GCC AAC  369

 S   F   L   Y   M   Q   K   T   L   R   Q   C   Q   E   Q   R   Q   C   H   C   129
TCT TTC CTC TAC ATG CAG AAA ACT CTG CGG CAA TGT CAG GAA CAG AGG CAG TGT CAC TGC  429

 R   Q   E   A   T   N   A   T   R   V   I   H   D   N   Y   D   Q   L   E   V   149
AGG CAG GAA GCC ACC AAT GCC ACC AGA GTC ATC CAT GAC AAC TAT GAT CAG CTG GAG GTC  489

 H   A   A   A   I   K   S   L   G   E   L   D   V   F   L   A   W   I   N   K   169
CAC GCT GCT GCC ATT AAA TCC CTG GGA GAG CTC GAC GTC TTT CTA GCC TGG ATT AAT AAG  549

 N   H   E   V   M   S   S   A   *                                               178
AAT CAT GAA GTA ATG TCC TCA GCT TGA                                              576

TGACAAGGAACCTGTATAGTGATCCAGGGATGAACACCCCCTGTGCGGTTTACTGTGGGAGACAGCCCACCTTGAAGGG  655

GAAGGAGATGGGGAAGGCCCCTTGCAGCTGAAAGTCCCACTGGCTGGCCTCAGGCTGTCTTATTCCGCTTGAAAATAGC  734

CAAAAAGTCTACTGTGGTATTTGTAATAAACTCTATCTGCTGAAAGGGCCTGCAGGCCATCCTGGGAGTAAAGGGCTGC  813

CTTCCCATCTAATTTATTGTGAAGTCATATAGTCCATGTCTGTGATGTGAGCCAAGTGATATCCTGTAGTACACATTGT  892

ACTGAGTGGTTTTTCTGAATAAATTCCATATTTTACCTATGAAAAAAAAAAAAAAAAAAAAAAACCAGCTGAGCGCCGG  971

TCGCTACCAAAGCCGAATTC                                                             991
```

Fig. 1

```
              1                                                       50
il10-human    ~MHSSALLCC LVLLTGVRAS PGQGTQSENS CTHFPGNLPN MLRDLRDAFS
il10-mouse    ~MPGSALLCC LLLLTGMRIS RGQYSREDNN CTHFPVGQSH MLLELRTAFS
il10-viral    ~MFRASLLCC LVLLAGVWAD NKYDSESGDD CPTLPTSLPH MLHELRAAFS
mda7-mouse    MSWGLQILPC LSLILLLWNQ VPGLEGQEFR FGSCQV.TGV VLPELWEAFW
mda7-human    ~~MQMVVLPC LGFTLLLWSQ VSGAQGQEFH FGPCQV.KGV VPQKLWEAFW
     italy    ~~~~~MKLQC VSLWLL..GT ILILCSVDNH GLRRCL.IST DMHHIEESFQ
 Consensus    -M-GSALLCC L-LLL--WA- VG-LSG-ENH C-H-PV-L-- MLHELREAFS

              51                                                     100
il10-human    RVKTFFQMKD QLDN..LLLK ESLLEDFKGY LGCQALSEMI QFYLEEVMPQ
il10-mouse    QVKTFFQTKD QLDN..ILLT DSLMQDFKGY LGCQALSEMI QFYLVEVMPQ
il10-viral    RVKTFFQMKD QLDN..MLLD GSLLEDFKGY LGCQALSEMI QFYLEEVMPQ
mda7-mouse    TVKNTVQTQD DITSIRLLKP .QVLRNVSGA ESCYLAHSLL KFYLNTVFKN
mda7-human    AVKDTMQAQD NITSARLLQQ .EVLQNVSDA ESCYLVHTLL EFYLKTVFKN
     italy    EIKRAIQAKD TFPNVTILST LETLQIIKPL DVCCVTKNLL AFYVDRVFKD
 Consensus    RVKTFFQ-KD QLDN-RLLLT -SLLQDFKGY LGCQALSE-- QFYLEEV--Q

              101                                                    150
il10-human    AENQDPD..I KAHVNSLGEN LKTLRLRLRR CHRFLPCENK SKAVEQ...V
il10-mouse    AEKHGPE..I KEHLNSLGEK LKTLRMRLRR CHRFLKCENK SKAVEQ...V
il10-viral    AENHSTD.QE KDKVNSLGEK LKTLRVRLRR CHRFLPCENK SKAVEQ...V
mda7-mouse    YHSKIAKFKV LRSFSTLANN FIVIMSQLQP SKDNSMLPIS ESAHQRFLLF
mda7-human    YHNRTVEVRT LKSFSTLANN FVLIVSQLQP SQENEMFSIR DSAHRRFLLF
     italy    HQE..PNPKI LRKISSIANS FLYMQKTLRQ CQEQRQCHCR QEATNATRVI
 Consensus    AENH-P--KI -R---SL--N -KTLRSRLRR CHRFL-CENK SKAVEQFLLV

              151                               187
il10-human    KNAFNKLQ.E KGIYKAMSEF DIFINYIEAY MTMKIRN
il10-mouse    KSDFNKLE.D QGVYKAMNEF DIFINCIEAY MMIKMKS
il10-viral    KSAFSKLQ.E KGVYKAMSEF DIFINYIEAY MTTKMKN
mda7-mouse    RRTFKQLDTE VALVKAFGEV DILLTWMQKF YHL~~~~
mda7-human    RRAFKQLDVE AALTKALGEV DILLTWMQKF YKL~~~~
     italy    HDNYDQLEVH AAAIKSLGEL DVFLAWINKN HEVMSSA
 Consensus    K-AF--L-VE ---YKAMGEF DIF-NWIE-Y MTLKMKN
```

Fig. 2

cgtccgccac gcgtccggac tagttctaga tcgcgagcgg ccgccctttt tttttttttt 60
ttggaagtcc taggactgat ctccaggacc agcactcttc tcccagccct tagggtcctg 120
ctcggccaag gccttccctg cc atg cga cct gtc agt gtc tgg cag tgg agc 172
ccc tgg ggg ctg ctg ctg tgc ctg ctg tgc agt tcg tgc ttg ggg tct 220
ccg tcc cct tcc acg ggc cct gag aag aag gcc ggg agc cag ggg ctt 268
cgg ttc cgg ctg gct ggc ttc ccc agg aag ccc tac gag ggc cgc gtg 316
gag ata cag cga gct ggt gaa tgg ggc acc atc tgc gat gat gac ttc 364
acg ctg cag gct gcc cac atc ctc tgc cgg gag ctg ggc ttc aca gag 412
gcc aca ggc tgg acc cac agt gcc aaa tat ggc cct gga aca ggc cgc 460
atc tgg ctg gac aac ttg agc tgc agt ggg acc gag cag agt gtg act 508
gaa tgt gcc tcc cgg ggc tgg ggg aac agt gac tgt acg cac gat gag 556
gat gct ggg gtc atc tgc aaa gac cag cgc ctc cct ggc ttc tcg gac 604
tcc aat gtc att gag gta gag cat cac ctg caa gtg gag gag gtg cga 652
att cga ccc gcc gtt ggg tgg ggc aga cga ccc ctg ccc gtg acg gag 700
ggg ctg gtg gaa gtc agg ctt cct gac ggc tgg tcg caa gtg tgc gac 748
aaa ggc tgg agc gcc cac aac agc cac gtg gtc tgc ggg atg ctg ggc 796
ttc ccc agc gaa aag agg gtc aac gcg gcc ttc tac agg ctg cta gcc 844
caa cgg cag caa cac tcc ttt ggt ctg cat ggg gtg gcg tgc gtg ggc 892
acg gag gcc cac ctc tcc ctc tgt tcc ctg gag ttc tat cgt gcc aat 940
gac acc gcc agg tgc cct ggg ggg ggc cct gca gtg gtg agc tgt gtg 988
cca ggc cct gtc tac gcg gca tcc agt ggc cag aag aag caa caa cag 1036
tcg aag cct cag ggg gag gcc cgt gtc cgt cta aag ggc ggc gcc cac 1084
cct gga gag ggc cgg gta gaa gtc ctg aag gcc agc aca tgg ggc aca 1132
gtc tgt gac cgc aag tgg gac ctg cat gca gcc agc gtg gtg tgt cgg 1180
gag ctg ggc ttc ggg agt gct cga gaa gct ctg agt ggc gct cgc atg 1228
ggg cag ggc atg ggt gct atc cac ctg agt gaa gtt cgc tgc tct gga 1276

Fig. 3A

cag gag ctc tcc ctc tgg aag tgc ccc cac aag aac atc aca gct gag 1324

gat tgt tca cat agc cag gat gcc ggg gtc cgg tgc aac cta cct tac 1372

act ggg gca gag acc agg atc cga ctc agt ggg ggc cgc agc caa cat 1420

gag ggg cga gtc gag gtg caa ata ggg gga cct ggg ccc ctt cgc tgg 1468

ggc ctc atc tgt ggg gat gac tgg ggg acc ctg gag gcc atg gtg gcc 1516

tgt agg caa ctg ggt ctg ggc tac gcc aac cac ggc ctg cag gag acc 1564

tgg tac tgg gac tct ggg aat ata aca gag gtg gtg atg agt gga gtg 1612

cgc tgc aca ggg act gag ctg tcc ctg gat cag tgt gcc cat cat ggc 1660

acc cac atc acc tgc aag agg aca ggg acc cgc ttc act gct gga gtc 1708

atc tgt tct gag act gca tca gat ctg ttg ctg cac tca gca ctg gtg 1756

cag gag acc gcc tac atc gaa gac cgg ccc ctg cat atg ttg tac tgt 1804

gct gcg gaa gag aac tgc ctg gcc agc tca gcc cgc tca gcc aac tgg 1852

ccc tat ggt cac cgg cgt ctg ctc cga ttc tcc tcc cag atc cac aac 1900

ctg gga cga gct gac ttc agg ccc aag gct ggg cgc cac tcc tgg gtg 1948

tgg cac gag tgc cat ggg cat tac cac agc atg gac atc ttc act cac 1996

tat gat atc ctc acc cca aat ggc acc aag gtg gct gag ggc cac aaa 2044

gct agt ttc tgt ctc gaa gac act gag tgt cag gag gat gtc tcc aag 2092

cgg tat gag tgt gcc aac ttt gga gag caa ggc atc act gtg ggt tgc 2140

tgg gat ctc tac cgg cat gac att gac tgt cag tgg att gac atc acg 2188

gat gtg aag cca gga aac tac att ctc cag gtt gtc atc aac cca aac 2236

ttt gaa gta gca gag agt gac ttt acc aac aat gca atg aaa tgt aac 2284

tgc aaa tat gat gga cat aga atc tgg gtg cac aac tgc cac att ggt 2332

gat gcc ttc agt gaa gag gcc aac agg agg ttt gaa cgc tac cct ggc 2380

cag acc agc aac cag att atc taagtgccac tgccctctgc aaaccaccac 2431

tggcccctaa tggcaggggt ctgaggctgc cattacctca ggagcttacc aagaaaccca 2491

tgtcagcaac cgcactcatc agaccatgca ctatggatgt ggaactgtca agcagaagtt 2551

Fig. 3B

```
ttcaccctcc ttcagaggcc agctgtcagt atctgtagcc aagcatggga atctttgctc 2611
ccaggcccag caccgagcag aacagaccag agcccaccac accacaaaga gcagcacctg 2671
actaactgcc cacaaaagat ggcagcagct cattttcttt aataggaggt caggatggtc 2731
agctccagta tctcccctaa gtttaggggg atacagcttt acctctagcc ttttggtggg 2791
ggaaaagatc cagccctccc acctcatttt ttactataat atgttgctag gtataatttt 2851
attttatata aaaagtgttt ctgtgattct tcagaaaaaa aaaaaaaaaa aaaaaaaaaa 2911
aaaaaaaaa                                                         2920
```

Fig. 3C

```
Met Arg Pro Val Ser Val Trp Gln Trp Ser Pro Trp Gly Leu Leu Leu
1               5                   10                  15

Cys Leu Leu Cys Ser Ser Cys Leu Gly Ser Pro Ser Pro Ser Thr Gly
            20                  25                  30

Pro Glu Lys Lys Ala Gly Ser Gln Gly Leu Arg Phe Arg Leu Ala Gly
        35                  40                  45

Phe Pro Arg Lys Pro Tyr Glu Gly Arg Val Glu Ile Gln Arg Ala Gly
    50                  55                  60

Glu Trp Gly Thr Ile Cys Asp Asp Asp Phe Thr Leu Gln Ala Ala His
65                  70                  75                  80

Ile Leu Cys Arg Glu Leu Gly Phe Thr Glu Ala Thr Gly Trp Thr His
                85                  90                  95

Ser Ala Lys Tyr Gly Pro Gly Thr Gly Arg Ile Trp Leu Asp Asn Leu
            100                 105                 110

Ser Cys Ser Gly Thr Glu Gln Ser Val Thr Glu Cys Ala Ser Arg Gly
        115                 120                 125

Trp Gly Asn Ser Asp Cys Thr His Asp Glu Asp Ala Gly Val Ile Cys
    130                 135                 140

Lys Asp Gln Arg Leu Pro Gly Phe Ser Asp Ser Asn Val Ile Glu Val
145                 150                 155                 160

Glu His His Leu Gln Val Glu Glu Val Arg Ile Arg Pro Ala Val Gly
                165                 170                 175

Trp Gly Arg Arg Pro Leu Pro Val Thr Glu Gly Leu Val Glu Val Arg
            180                 185                 190

Leu Pro Asp Gly Trp Ser Gln Val Cys Asp Lys Gly Trp Ser Ala His
        195                 200                 205

Asn Ser His Val Val Cys Gly Met Leu Gly Phe Pro Ser Glu Lys Arg
    210                 215                 220

Val Asn Ala Ala Phe Tyr Arg Leu Leu Ala Gln Arg Gln Gln His Ser
225                 230                 235                 240

Phe Gly Leu His Gly Val Ala Cys Val Gly Thr Glu Ala His Leu Ser
                245                 250                 255

Leu Cys Ser Leu Glu Phe Tyr Arg Ala Asn Asp Thr Ala Arg Cys Pro
            260                 265                 270
```

Fig. 4A

Gly Gly Gly Pro Ala Val Val Ser Cys Val Pro Gly Pro Val Tyr Ala
275 280 285

Ala Ser Ser Gly Gln Lys Lys Gln Gln Gln Ser Lys Pro Gln Gly Glu
290 295 300

Ala Arg Val Arg Leu Lys Gly Gly Ala His Pro Gly Glu Gly Arg Val
305 310 315 320

Glu Val Leu Lys Ala Ser Thr Trp Gly Thr Val Cys Asp Arg Lys Trp
325 330 335

Asp Leu His Ala Ala Ser Val Val Cys Arg Glu Leu Gly Phe Gly Ser
340 345 350

Ala Arg Glu Ala Leu Ser Gly Ala Arg Met Gly Gln Gly Met Gly Ala
355 360 365

Ile His Leu Ser Glu Val Arg Cys Ser Gly Gln Glu Leu Ser Leu Trp
370 375 380

Lys Cys Pro His Lys Asn Ile Thr Ala Glu Asp Cys Ser His Ser Gln
385 390 395 400

Asp Ala Gly Val Arg Cys Asn Leu Pro Tyr Thr Gly Ala Glu Thr Arg
405 410 415

Ile Arg Leu Ser Gly Gly Arg Ser Gln His Glu Gly Arg Val Glu Val
420 425 430

Gln Ile Gly Gly Pro Gly Pro Leu Arg Trp Gly Leu Ile Cys Gly Asp
435 440 445

Asp Trp Gly Thr Leu Glu Ala Met Val Ala Cys Arg Gln Leu Gly Leu
450 455 460

Gly Tyr Ala Asn His Gly Leu Gln Glu Thr Trp Tyr Trp Asp Ser Gly
465 470 475 480

Asn Ile Thr Glu Val Val Met Ser Gly Val Arg Cys Thr Gly Thr Glu
485 490 495

Leu Ser Leu Asp Gln Cys Ala His His Gly Thr His Ile Thr Cys Lys
500 505 510

Arg Thr Gly Thr Arg Phe Thr Ala Gly Val Ile Cys Ser Glu Thr Ala
515 520 525

Ser Asp Leu Leu Leu His Ser Ala Leu Val Gln Glu Thr Ala Tyr Ile
530 535 540

Fig. 4B

Glu Asp Arg Pro Leu His Met Leu Tyr Cys Ala Ala Glu Glu Asn Cys
545   550   555   560

Leu Ala Ser Ser Ala Arg Ser Ala Asn Trp Pro Tyr Gly His Arg Arg
                565   570   575

Leu Leu Arg Phe Ser Ser Gln Ile His Asn Leu Gly Arg Ala Asp Phe
            580   585   590

Arg Pro Lys Ala Gly Arg His Ser Trp Val Trp His Glu Cys His Gly
        595   600   605

His Tyr His Ser Met Asp Ile Phe Thr His Tyr Asp Ile Leu Thr Pro
    610   615   620

Asn Gly Thr Lys Val Ala Glu Gly His Lys Ala Ser Phe Cys Leu Glu
625   630   635   640

Asp Thr Glu Cys Gln Glu Asp Val Ser Lys Arg Tyr Glu Cys Ala Asn
                645   650   655

Phe Gly Glu Gln Gly Ile Thr Val Gly Cys Trp Asp Leu Tyr Arg His
            660   665   670

Asp Ile Asp Cys Gln Trp Ile Asp Ile Thr Asp Val Lys Pro Gly Asn
        675   680   685

Tyr Ile Leu Gln Val Val Ile Asn Pro Asn Phe Glu Val Ala Glu Ser
    690   695   700

Asp Phe Thr Asn Asn Ala Met Lys Cys Asn Cys Lys Tyr Asp Gly His
705   710   715   720

Arg Ile Trp Val His Asn Cys His Ile Gly Asp Ala Phe Ser Glu Glu
                725   730   735

Ala Asn Arg Arg Phe Glu Arg Tyr Pro Gly Gln Thr Ser Asn Gln Ile
            740   745   750

Ile
753

Fig. 4C

```
atgcgacctg tcagtgtctg gcagtggagc ccctgggggc tgctgctgtg cctgctgtgc 60
agttcgtgct tggggtctcc gtccccttcc acgggccctg agaagaaggc cgggagccag 120
gggcttcggt tccggctggc tggcttcccc aggaagccct acgagggccg cgtggagata 180
cagcgagctg gtgaatgggg caccatctgc gatgatgact tcacgctgca ggctgcccac 240
atcctctgcc gggagctggg cttcacagag gccacaggct ggacccacag tgccaaatat 300
ggccctggaa caggccgcat ctggctggac aacttgagct gcagtgggac cgagcagagt 360
gtgactgaat gtgcctcccg ggggctgggg aacagtgact gtacgcacga tgaggatgct 420
ggggtcatct gcaaagacca gcgcctccct ggcttctcgg actccaatgt cattgaggta 480
gagcatcacc tgcaagtgga ggaggtgcga attcgacccg ccgttgggtg gggcagacga 540
cccctgcccg tgacggaggg gctggtggaa gtcaggcttc ctgacggctg gtcgcaagtg 600
tgcgacaaag gctggagcgc ccacaacagc cacgtggtct gcgggatgct gggcttcccc 660
agcgaaaaga gggtcaacgc ggccttctac aggctgctag cccaacggca gcaacactcc 720
tttggtctgc atggggtggc gtgcgtgggc acggaggccc acctctccct ctgttccctg 780
gagttctatc gtgccaatga caccgccagg tgccctgggg ggggccctgc agtggtgagc 840
tgtgtgccag gccctgtcta cgcggcatcc agtggccaga agaagcaaca acagtcgaag 900
cctcaggggg aggcccgtgt ccgtctaaag ggcggcgccc accctggaga gggccgggta 960
gaagtcctga aggccagcac atggggcaca gtctgtgacc gcaagtggga cctgcatgca 1020
gccagcgtgg tgtgtcggga gctgggcttc gggagtgctc gagaagctct gagtggcgct 1080
cgcatggggc agggcatggg tgctatccac ctgagtgaag ttcgctgctc tggacaggag 1140
ctctccctct ggaagtgccc ccacaagaac atcacagctg aggattgttc acatagccag 1200
gatgccgggg tccggtgcaa cctaccttac actggggcag agaccaggat ccgactcagt 1260
gggggccgca gccaacatga ggggcgagtc gaggtgcaaa taggggggacc tgggcccctt 1320
cgctggggcc tcatctgtgg ggatgactgg gggaccctgg aggccatggt ggcctgtagg 1380
caactgggtc tgggctacgc caaccacggc ctgcaggaga cctggtactg ggactctggg 1440
aatataacag aggtggtgat gagtggagtg cgctgcacag ggactgagct gtccctggat 1500
```

Fig. 5A

```
cagtgtgccc atcatggcac ccacatcacc tgcaagagga cagggacccg cttcactgct 1560
ggagtcatct gttctgagac tgcatcagat ctgttgctgc actcagcact ggtgcaggag 1620
accgcctaca tcgaagaccg gcccctgcat atgttgtact gtgctgcgga agagaactgc 1680
ctggccagct cagcccgctc agccaactgg ccctatggtc accggcgtct gctccgattc 1740
tcctcccaga tccacaacct gggacgagct gacttcaggc ccaaggctgg gcgccactcc 1800
tgggtgtggc acgagtgcca tgggcattac cacagcatgg acatcttcac tcactatgat 1860
atcctcaccc caaatggcac caaggtggct gagggccaca aagctagttt ctgtctcgaa 1920
gacactgagt gtcaggagga tgtctccaag cggtatgagt gtgccaactt tggagagcaa 1980
ggcatcactg tgggttgctg ggatctctac cggcatgaca ttgactgtca gtggattgac 2040
atcacggatg tgaagccagg aaactacatt ctccaggttg tcatcaaccc aaactttgaa 2100
gtagcagaga gtgactttac caacaatgca atgaaatgta actgcaaata tgatggacat 2160
agaatctggg tgcacaactg ccacattggt gatgccttca gtgaagaggc caacaggagg 2220
tttgaacgct accctggcca gaccagcaac cagattatc                        2259
```

Fig. 5B

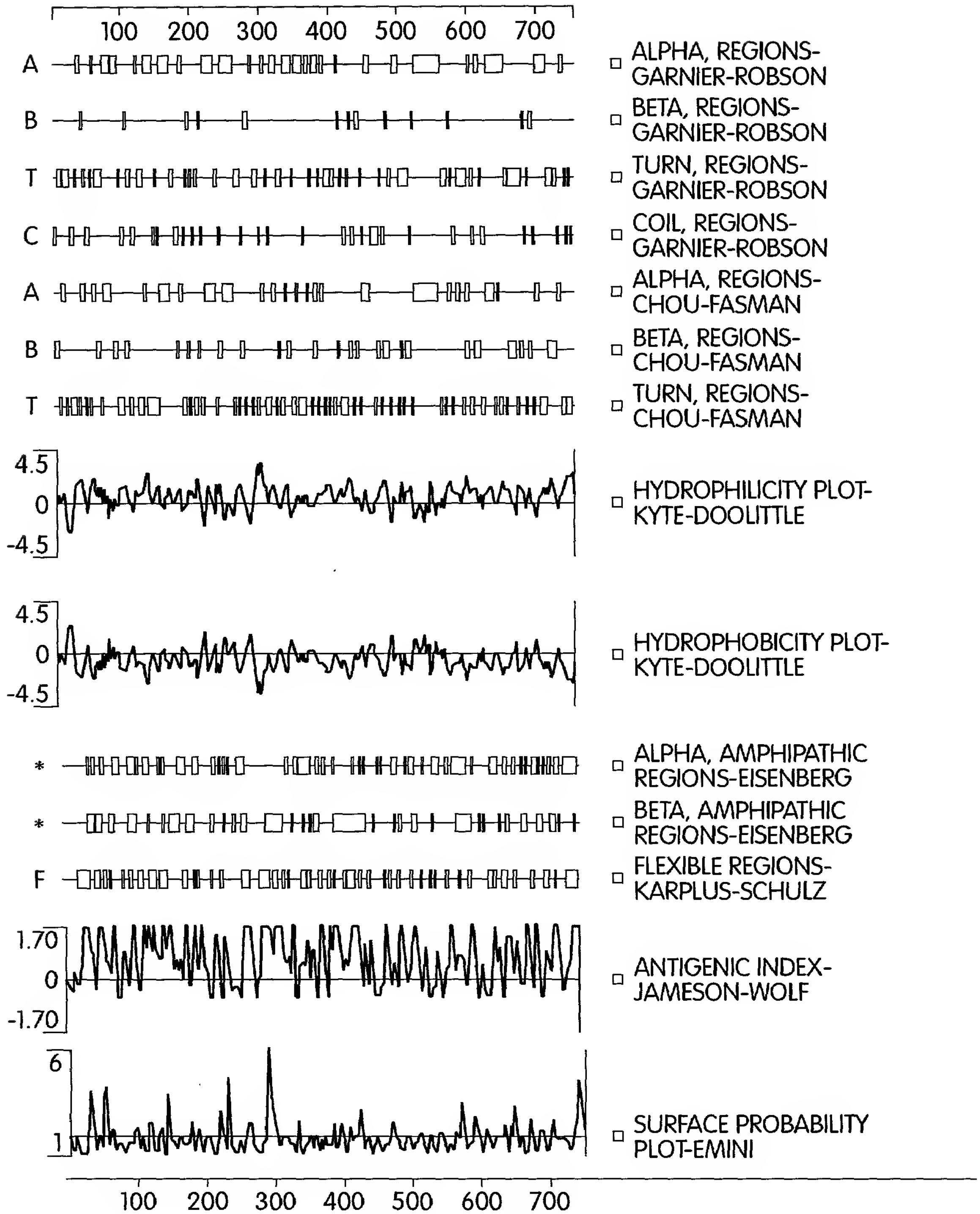
100 200 300 400 500 600 700
A
ALPHA, REGIONS-GARNIER-ROBSON
B
BETA, REGIONS-GARNIER-ROBSON
T
TURN, REGIONS-GARNIER-ROBSON
C
COIL, REGIONS-GARNIER-ROBSON
A
ALPHA, REGIONS-CHOU-FASMAN
B
BETA, REGIONS-CHOU-FASMAN
T
TURN, REGIONS-CHOU-FASMAN
4.5
0
-4.5
HYDROPHILICITY PLOT-KYTE-DOOLITTLE
4.5
0
-4.5
HYDROPHOBICITY PLOT-KYTE-DOOLITTLE
*
ALPHA, AMPHIPATHIC REGIONS-EISENBERG
*
BETA, AMPHIPATHIC REGIONS-EISENBERG
F
FLEXIBLE REGIONS-KARPLUS-SCHULZ
1.70
0
-1.70
ANTIGENIC INDEX-JAMESON-WOLF
6
1
SURFACE PROBABILITY PLOT-EMINI
100 200 300 400 500 600 700

Fig. 6

```
                1                                                          60
LOX             MRFA--------WTVLLLGPLQ-----------LCALVHCAPPAAGQQQP----------
huLOL           MALA--------RGSRQLGALV-------WGACLCVHVH------GQQAQ----------
huLor           MERPLCSHLCSCLAMLALLSPLSLAQYDSWPHYPEYFQQPAPEYHQPQAPANVAKIQLRL
muLor-2         M-RAVSVWYCCPWGLLLLHCL-C----------SFSVGSPSPS-ISPEKKVGSQGLRFRL
huLor-2         M-RPVSVWQWSPWGLLL--CLLC----------SSCLGSPSPS-TGPEKKAGSQGLRFRL

                61                                                        120
LOX             ---PREPPAAPGAWRQQIQWENN-GQVFSL-----LSLGSQY------------------
huLOL           ---P-GQGSDPARWRQLIQWENN-GQVYSL-----LNSGSEYVPA-----GPQRSESSSR
huLor           AGQKRKHSEGRVEVYYDGQWGTVCDDDFSIHAAHVVCRELGYVEAKSWTASSSYGKGEGP
muLor-2         AGFPRKPYEGRVEIQRAGEWGTICDDDFTLQAAHVLCRELGFTEATGWTHSAKYGPGTGR
huLor-2         AGFPRKPYEGRVEIQRAGEWGTICDDDFTLQAAHILCRELGFTEATGWTHSAKYGPGTGR

                121                                                       180
LOX             ------------------------QPQRRRDPGAA-------VPG---AANASAQQPRTP
huLOL           VLLA--------GAPQAQQRRSHGSPRRRQAPSLP-------LPG-RVGSDTVRGQARHP
huLor           IWLDNLHCTGNEATLAACTSNGWGVTDCKHTEDVGVVCSDKRIPGFKFDNSLINQIENLN
muLor-2         IWLDNLSCRGTEGSVTECASRGWGNSDCTHDEDAGVICKDQRLPGF--SDSNVIEVEH-Q
huLor-2         IWLDNLSCSGTEQSVTECASRGWGNSDCTHDEDAGVICKDQRLPGF--SDSNVIEVEH-H

                181                                                       240
LOX             ILL--IRD----N---------------RTAAG------RTRTAGSSGVTAG--------
huLOL           FGFGQVPD----NWREVAVGDSTGMALARTSVS------QQRHGGSASSVSAS-AFAST-
huLor           IQVEDIRIRAILSTYRKRTPVMEGYVEVKEGKTWKQICDKHWTAKNSRVVCGMFGFPGER
muLor-2         LQVEEVRLRPAVEWGRRPLPVTEGLVEVRLPEGWSQVCDKGWSAHNSHVVCGMLGFPGEK
huLor-2         LQVEEVRIRPAVGWGRRPLPVTEGLVEVRLPDGWSQVCDKGWSAHNSHVVCGMLGFPSEK

                241                                                       300
LOX             -------RP-RPTARHWF---------------------QAGY------------STSRA
huLOL           ------YRQ-QPSYPQQFPY------------------PQAPF----VSQYENYDPASRT
huLor           TYNTKVYKNFASRRKQRYWPFSMDCTGTEAHISSCKLGPQVSLDPMKNVTCENGLPAVVS
muLor-2         RVNMAFYRMLAQKKQHSFGLHSVACVGTEAHLSLCSLE---FYRANDTTRCSGGNPAVVS
huLor-2         RVNAAFYRLLAQRQQHSFGLHGVACVGTEAHLSLCSLE---FYRANDTARCPGGGPAVVS

                301                                                       360
LOX             -------------------REAGPSR----AENQTAPGEVPAL------------SNLRP
huLOL           YDQGFVY-----------YRPAGGGV----GAGAAAVASAGVI------------YPYQP
huLor           CVPGQVFSPDGPSRFRKAYKPE-QPLVRLRGGAYIGEGRVEVLKNGEWGTVCDDKWDLVS
muLor-2         CVLGPLYATFTGQKKQQHSKPQGEARVRLKGGAHQGEGRVEVLKAGTWGTVCDRKWDLQA
huLor-2         CVPGPVYAASSGQKKQQQSKPQGEARVRLKGGAHPGEGRVEVLKASTWGTVCDRKWDLHA

                361                                                       420
LOX             PS------------------RVDGMVGDD--------------------PYNP-------
huLOL           RA------------------RYEEYGGGEELPEYPPQG----FYPAPERPYVPPPPPPPD
huLor           ASVVCRELGFGSAKEAVTGSRLGQGIGPIHLNEIQCTGNEKSIIDCKFNA-ESQGCNHEE
muLor-2         ASVVCPELGFGTAREALSGARMGQGMGAIHLSEVRCSGQEPSLWRCPSKNITAEDCSHSQ
huLor-2         ASVVCRELGFGSAREALSGARMGQGMGAIHLSEVRCSGQELSLWKCPHKNITAEDCSHSQ
```

Fig. 7A

```
        421                                                        480
LOX     -----YK---YSDDNPYYNYYDTYERPRPG-----------GRYRP---------GYGTG
huLOL   GLDRRYSHSLYSEGTPGFE--QAYPDPGPEAAQAHGGDPRLGWYPPYANP--PPEAYGPP
huLor   DAGVRCNTP-AMGLQKKLRLNGGRNPYEGRVEVLVERNGSLVWGMVCGQNWGIVEAMVVC
muLor-2 DAGVRCNLP-YTGVETKIRLSGGRSRYEGRVEVQIGIPGHLRWGLICGDDWGTLEAMVAC
huLor-2 DAGVRCNLP-YTGAETRIRLSGGRSQHEGRVEVQIGGPGPLRWGLICGDDWGTLEAMVAC

        481                                                        540
LOX     ------Y----------------FQ---------------------------------Y
huLOL   RALEPPY-----------------LPVRSSDTPPPGGE-------RNGAQQGRLSVGSVY
huLor   RQLGLGFASNAFQETWYWHGDVNSNKVVMSGVKCSGTELSLAHCRHDGEDVACPQGGVQY
muLor-2 RQLGLGYANHGLQETWYWDSG-NVTEVVMSGVRCTGSELSLNQCAHHSSHITCKKTGTRF
huLor-2 RQLGLGYANHGLQETWYWDSG-NITEVVMSGVRCTGTELSLDQCAHHGTHITCKRTGTRF

        541                                                        600
LOX     --------GLPDLVADPYYIQASTYVQKMSMYNLRCAAEENCLASTAYRADVRDYDHRVL
huLOL   RPNQN-GRGLPDLVPDPNYVQASTYVQRAHLYSLRCAAEEKCLASTAYAPEATDYDVRVL
huLor   GAGVACSETAPDLVLNAEMVQQTTYLEDRPMFMLQCAMEENCLSASAAQTD-PTTGYRRL
muLor-2 TAGVICSETASDLLLHSALVQETAYIEDRPLHMLYCAAEENCLASSARSAN-WPYGHRRL
huLor-2 TAGVICSETASDLLLHSALVQETAYIEDRPLHMLYCAAEENCLASSARSAN-WPYGHRRL

        601                                                        660
LOX     LRFPQRVKNQGTSDFLPSRPRYSWEWHSCHQHYHSMDEFSHYDLLDANTQRRVAEGHKAS
huLOL   LRFPQRVKNQGTADFLPNRPRHTWEWHSCHQHYHSMDEFSHYDLLDAATGKKVAEGHKAS
huLor   LRFSSQIHNNGQSDFRPKNGRHAWIWHDCHRHYHSMEVFTHYDLLNLN-GTKVAEGHKAS
muLor-2 LRFSSQIHNLGRADFRPKAGRHSWVWHECHGHYHSMDIFTHYDILTPN-GTKVAEGHKAS
huLor-2 LRFSSQIHNLGRADFRPKAGRHSWVWHECHGHYHSMDIFTHYDILTPN-GTKVAEGHKAS

        661                                                        720
LOX     FCLEDTSCDYGYHRRFACTAHT-QGLSPGCYDTYGADIDCQWIDITDVKPGNYILKVSVN
huLOL   FCLEDSTCDFGNLKRYACTSHT-QGLSPGCYDTYNADIDCQWIDITDVQPGNYILKVHVN
huLor   FCLEDTECEGDIQKNYECANFGDQGITMGCWDMYRHDIDCQWVDITDVPPGDYLFQVVIN
muLor-2 FCLEDTECQEDVSKRYECANFGEQGITVGCWDLYRHDIDCQWIDITDVKPGNYILQVVIN
huLor-2 FCLEDTECQEDVSKRYECANFGEQGITVGCWDLYRHDIDCQWIDITDVKPGNYILQVVIN

        721                                                       779
LOX     PSYLVPESDYTNNVVRCDIRYTGHHAYASGCTI----------------------SPY
huLOL   PKYIVLESDFTNNVVRCNIHYTGRYVSATNCKI-----------------------VQS
huLor   PNFEVAESDYSNNIMKCRSRYDGHRIWMYNCHIGGSFSEETEKKFEHFSGLLNNQLSPQ
muLor-2 PNFEVAESDFTNNAMKCNCKYDGHRIWVHNCHIGDAFSEEANRRFERYPGQTSNQIV--
huLor-2 PNFEVAESDFTNNAMKCNCKYDGHRIWVHNCHIGDAFSEEANRRFERYPGQTSNQII--
```

Fig. 7B

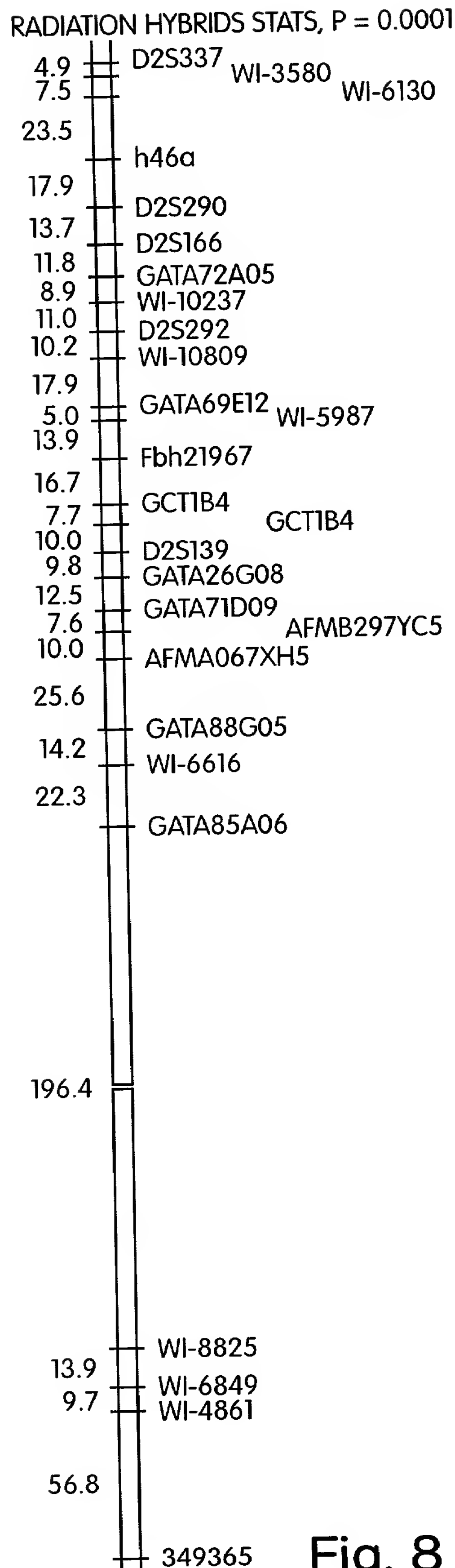
RADIATION HYBRIDS STATS, P = 0.0001
4.9
7.5
D2S337
WI-3580
WI-6130
23.5
h46a
17.9
D2S290
13.7
D2S166
11.8
GATA72A05
8.9
WI-10237
11.0
D2S292
10.2
WI-10809
17.9
GATA69E12
WI-5987
5.0
13.9
Fbh21967
16.7
GCT1B4
7.7
GCT1B4
10.0
D2S139
9.8
GATA26G08
12.5
GATA71D09
7.6
AFMB297YC5
10.0
AFMA067XH5
25.6
GATA88G05
14.2
WI-6616
22.3
GATA85A06
196.4
WI-8825
13.9
WI-6849
9.7
WI-4861
56.8
349365

Fig. 8

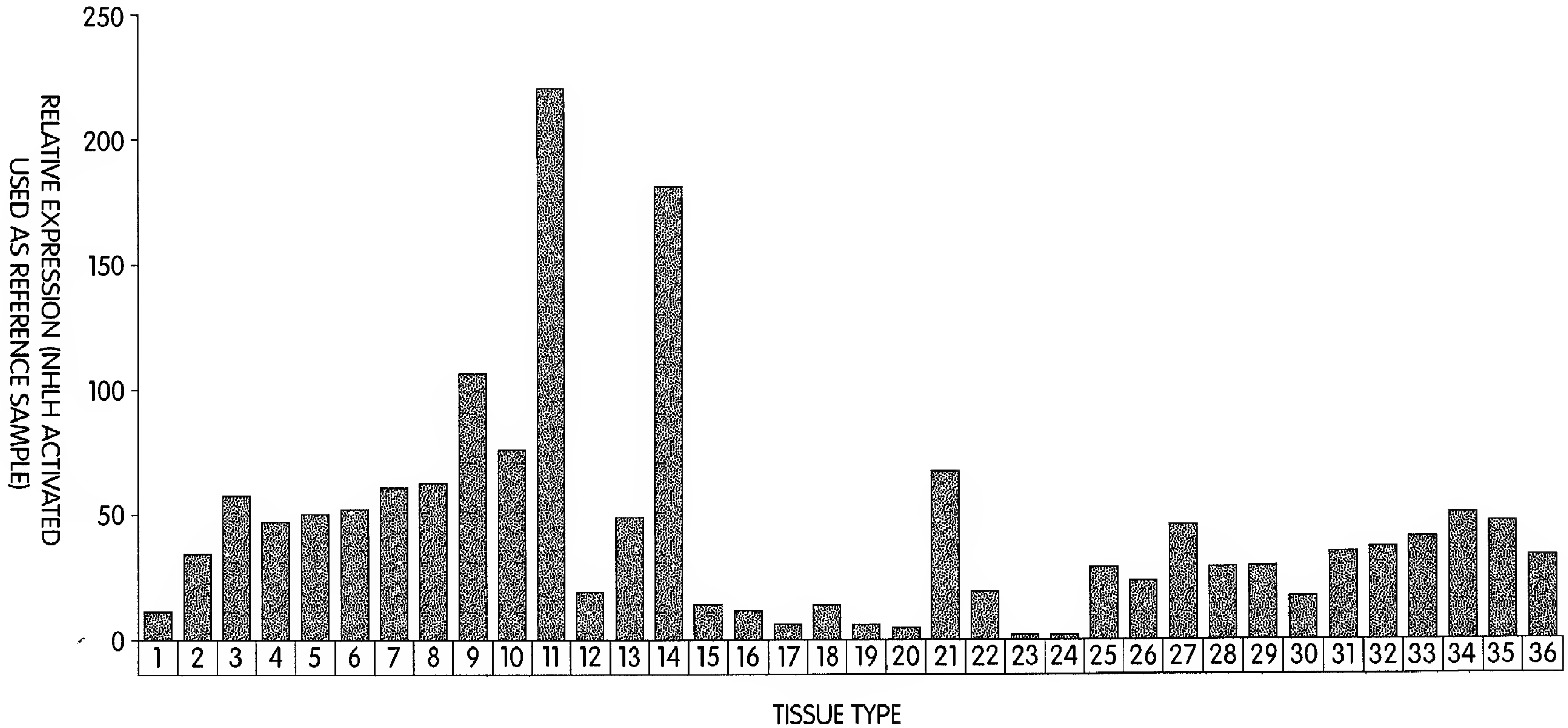
RELATIVE EXPRESSION (NHLH ACTIVATED USED AS REFERENCE SAMPLE)
250
200
150
100
50
0
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36
TISSUE TYPE

Fig. 9

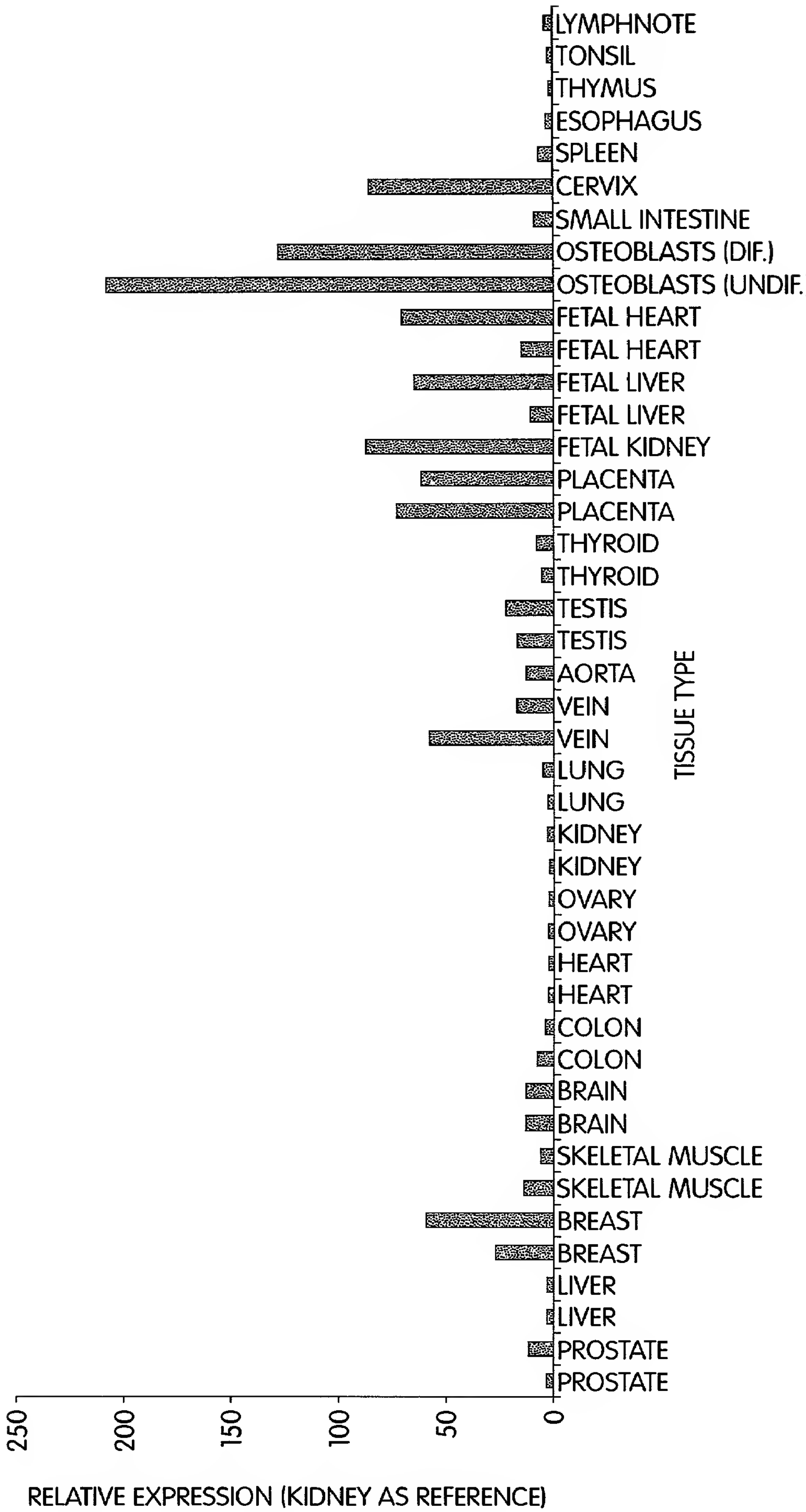
LYMPHNOTE
TONSIL
THYMUS
ESOPHAGUS
SPLEEN
CERVIX
SMALL INTESTINE
OSTEOBLASTS (DIF.)
OSTEOBLASTS (UNDIF.)
FETAL HEART
FETAL HEART
FETAL LIVER
FETAL LIVER
FETAL KIDNEY
PLACENTA
PLACENTA
THYROID
THYROID
TESTIS
TESTIS
AORTA
VEIN
VEIN
LUNG
LUNG
KIDNEY
KIDNEY
OVARY
OVARY
HEART
HEART
COLON
COLON
BRAIN
BRAIN
SKELETAL MUSCLE
SKELETAL MUSCLE
BREAST
BREAST
LIVER
LIVER
PROSTATE
PROSTATE
TISSUE TYPE
250
200
150
100
50
0
RELATIVE EXPRESSION (KIDNEY AS REFERENCE)

Fig. 10

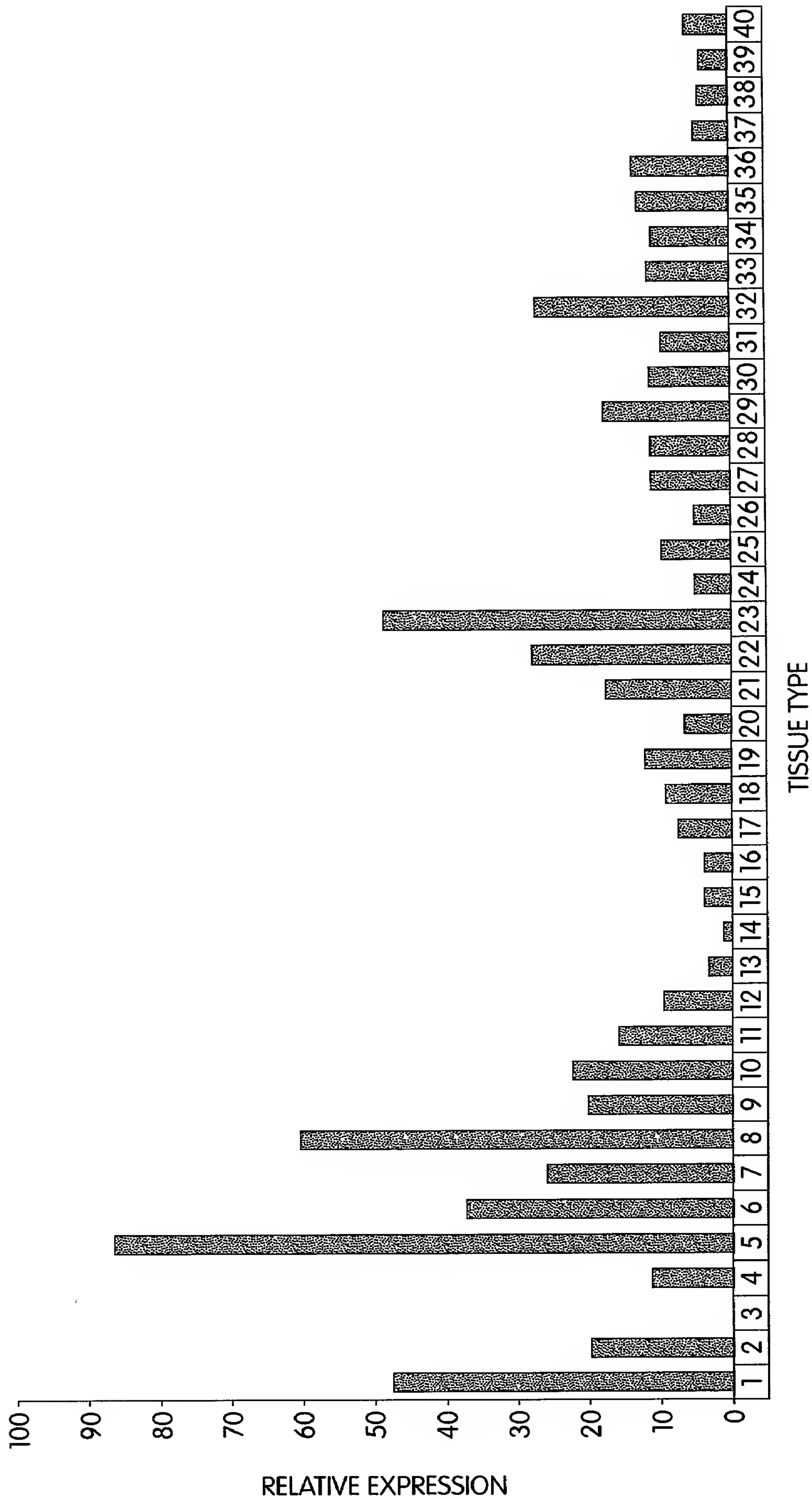
RELATIVE EXPRESSION
0
10
20
30
40
50
60
70
80
90
100
TISSUE TYPE
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40

Fig. 11

GAATTCGGCACGAGGGCCGGCACCCCCGCGCCACCCCAGCCTCAAACTGCAGTCCGGCGCCGCGGGGCAGGACAAGGGG 79

M A L K V L P L H R T V L 13
AAGGAATAAACACGTTTGGTGAGAGCC ATG GCA CTC AAG GTC CTA CCT CTA CAC AGG ACG GTG CTC 145

F A A I L F L L H L A C K V S C E T G D 33
TTC GCT GCC ATT CTC TTC CTA CTC CAC CTG GCA TGT AAA GTG AGT TGC GAA ACC GGA GAT 205

C R Q Q E F K D R S G N C V L C K Q C G 53
TGC AGG CAG CAG GAA TTC AAG GAT CGA TCT GGA AAC TGT GTC CTC TGC AAA CAG TGC GGA 265

P G M E L S K E C G F G Y G E D A Q C V 73
CCT GGC ATG GAG TTG TCC AAG GAA TGT GGC TTC GGC TAT GGG GAG GAT GCA CAG TGT GTG 325

P C R P H R F K E D W G F Q K C K P C A 93
CCC TGC AGG CCG CAC CGG TTC AAG GAA GAC TGG GGT TTC CAG AAG TGT AAG CCA TGT GCG 385

D C A L V N R F Q R A N C S H T S D A V 113
GAC TGT GCG CTG GTG AAC CGC TTT CAG AGG GCC AAC TGC TCA CAC ACC AGT GAT GCT GTC 445

C G D C L P G F Y R K T K L V G F Q D M 133
TGC GGG GAC TGC CTG CCA GGA TTT TAC CGG AAG ACC AAA CTG GTT GGT TTT CAA GAC ATG 505

Fig. 12A

E C V P C G D P P P P Y E P H C T S K V 153
GAG TGT GTG CCC TGC GGA GAC CCA CCT CCT CCC TAC GAA CCA CAC TGT ACC AGC AAG GTG 565

N L V K I S S T V S S P R D T A L A A V 173
AAC CTT GTG AAG ATC TCC TCC ACC GTC TCC AGC CCT CGG GAC ACG GCG CTG GCT GCC GTC 625

I C S A L A T V L L A L L I L C V I Y C 193
ATC TGC AGT GCT CTG GCC ACG GTG CTG CTC GCC CTG CTC ATC CTG TGT GTC ATC TAC TGC 685

K R Q F M E K K P S C K L P S L C L T V 213
AAG AGG CAG TTC ATG GAG AAG AAA CCC AGC TGT AAG CTC CCA TCC CTC TGT CTC ACT GTG 745

K * 215
AAG TGA 751

GCTTGTTAGCATTGTCACCCAAGAGTTCTCAAGACACCTGGCTGAGACCTAAGACCTTTAGAGCATCAACAGCTACTTA 830

GAATACAAGATGCAGGAAAACGAGCCTCTTCAGGAATCTCAGGGCCTCCTAGGGATGCTGGCAAGGCTGTGATGTCTCA 909

AGGCTACCAGGAAAAAATAAAAGTTGTCTATACCCTAAAAAAAAAAAAAAAAAAAAAAAAACATGCGGCCGC 981

Fig. 12B

```
GAATTCGGCACGAGGGCGTTTGGCGCGGAAGTGCTACCAAGCTGCGGAAAGCGTGAGTCTGGAGCACAGCACTGGCGAG 79

                               M   A   L   K   V   L   P   L   H   R   T   V       12
TAGCAGGAATAAACACGTTTGGTGAGAGCC ATG GCA CTC AAG GTC CTA CCT CTA CAC AGG ACG GTG    145

 L   F   A   A   I   L   F   L   L   H   L   A   C   K   V   S   C   E   T   G     32
CTC TTC GCT GCC ATT CTC TTC CTA CTC CAC CTG GCA TGT AAA GTG AGT TGC GAA ACC GGA   205

 D   C   R   Q   Q   E   F   K   D   R   S   G   N   C   V   L   C   K   Q   C     52
GAT TGC AGG CAG CAG GAA TTC AAG GAT CGA TCT GGA AAC TGT GTC CTC TGC AAA CAG TGC   265

 G   P   G   M   E   L   S   K   E   C   G   F   G   Y   G   E   D   A   Q   C     72
GGA CCT GGC ATG GAG TTG TCC AAG GAA TGT GGC TTC GGC TAT GGG GAG GAT GCA CAG TGT   325

 V   P   C   R   P   H   R   F   K   E   D   W   G   F   Q   K   C   K   P   C     92
GTG CCC TGC AGG CCG CAC CGG TTC AAG GAA GAC TGG GGT TTC CAG AAG TGT AAG CCA TGT   385

 A   D   C   A   L   V   N   R   F   Q   R   A   N   C   S   H   T   S   D   A    112
GCG GAC TGT GCG CTG GTG AAC CGC TTT CAG AGG GCC AAC TGC TCA CAC ACC AGT GAT GCT   445

 V   C   G   D   C   L   P   G   F   Y   R   K   T   K   L   V   G   F   Q   D    132
GTC TGC GGG GAC TGC CTG CCA GGA TTT TAC CGG AAG ACC AAA CTG GTT GGT TTT CAA GAC   505

 M   E   C   V   P   C   G   D   P   P   P   P   Y   E   P   H   C   E   *        151
ATG GAG TGT GTG CCC TGC GGA GAC CCA CCT CCT CCC TAC GAA CCA CAC TGT GAG TGA       562

TGTGCCAAGTGGCAGCAGACCTTTAAAAAAAAAAGAAAAAAAAACAAACAAAAACAAAAAAAAAAAAAAAAAAAAAAAA 641

ATTTCCGCGGCCGC                                                                   655
```

Fig. 13

```
         MALKVLPLHRTVLFAAILFLLHLACKVSCETGDCRQQEFKDRSGNCVLCK  Majority
                  10        20        30        40        50
1        MALKVLPLHRTVLFAAILFLLHLACKVSCETGDCRQQEFKDRSGNCVLCK  muT127a
1        MALKVLPLHRTVLFAAILFLLHLACKVSCETGDCRQQEFKDRSGNCVLCK  muT127b
1        MYVWVQQ-------PTALLLLALTLGVTARRLNCVKHTYPS-GHKC--CR  ox40

         QCGPGMELSKECGFGYGEDAQCVPCRPHRFKEDWGFQKCKPCADCALVNR  Majority
                  60        70        80        90       100
51       QCGPGMELSKECGFGYGEDAQCVPCRPHRFKEDWGFQKCKPCADCALVNR  muT127a
51       QCGPGMELSKECGFGYGEDAQCVPCRPHRFKEDWGFQKCKPCADCALVNR  muT127b
41       ECQPGHGMVSRC--DHTRDTLCHPCETGFYNEAVNYDTCKQCTQCNHRSG  ox40

         FQ-RANCSHTSDAVCGDCLPGFYRKTKLVGFQ-DMECVPCGDPPPPYEPH  Majority
                 110       120       130       140       150
101      FQ-RANCSHTSDAVCGDCLPGFYRKTKLVGFQ-DMECVPCGDPPPPYEPH  muT127a
101      FQ-RANCSHTSDAVCGDCLPGFYRKTKLVGFQ-DMECVPCGDPPPPYEPH  muT127b
89       SELKQNCTPTQDTVC-RCRPGTQPRQD-SGYKLGVDCVPC--PPGHFSPG  ox40
```

Fig. 14A

```
     ----------------------------CEXXXXLXXXXXXXXXXXXXX  Majority
              160       170       180       190       200
149  ----------------------------CTSKVNLVKI-----------  muT127a
149  ----------------------------CE.                   muT127b
135  NNQACKPWTNCTLSGKQTRHPASDSLDAVCEDRSLLATLLWETQRPTFRP  ox40

     XXXXXXXXXXXXXXXXXXXTXXXPXXXAXAXXXXXXLXXXXXLXXLLXLX  Majority
              210       220       230       240       250
159  ----------------SSTVSSPRDTALAAVICSALATV--LLALLILC  muT127a
151                                                      muT127b
185  TTVQSTTVWPRTSELPSPPTLVTPEGPAFAVLLGLGLGLLAPLTVLLALY  ox40

     XXXXXXXXXXXXXXCXXXSXXXXXXXXXXXXXXXXXK-              Majority
              260       270       280
190  VIYCKRQFMEKKPSCKLPSLCLTV------------K.              muT127a
151                                                      muT127b
235  LLRKAWRLPNTPKPCWGNSFRTPIQEEHTDAHFTLAKI              ox40
```

Fig. 14B

```
 FASTA searches a protein or DNA sequence data bank
 version 2.0u53 July, 1996
Please cite:
 W.R. Pearson & D.J. Lipman PNAS (1988) 85:2444-2448

 inputs/nb589712.tmp :  215 aa
 > T127Atm473200aa: 215 aa
 vs  library
 searching inputs/nb782215.tmp library

    423 residues in     1 sequence
The best scores are:                                  initn init1 opt
 Patent Protein W70387 - (untitled)                     982 982   982

>> Patent Protein W70387 - (untitled)                     (423 aa)
initn:  982  init1:  982  opt:  982
Smith-Waterman score: 982;    85.7% identity in 203 aa overlap

                10        20        30        40        50        60

 T127A MALKVLPLHRTVLFAAILFLLHLACKVSCETGDCRQQEFKDRSGNCVLCKQCGPGMELSK

       X:::::  .  ..:. ...:  :.:::.:::::::::::.::::::: :.::::::::::

       MALKVLLEQEKTFFTLLVLLGYLSCKVTCETGDCRQQEFRDRSGNCVPCNQCGPGMELSK

                10        20        30        40        50        60
```

Fig. 15A

```
               70        80        90       100       110       120
T127A ECGFGYGEDAQCVPCRPHRFKEDWGFQKCKPCADCALVNRFQRANCSHTSDAVCGDCLPG
      ::::::::::::: :: ::::::::::::::: :::.:::::.:::: ::::.:::::::
      ECGFGYGEDAQCVTCRLHRFKEDWGFQKCKPCLDCAVVNRFQKANCSATSDAICGDCLPG
               70        80        90       100       110       120

              130       140       150       160       170       180
T127A FYRKTKLVGFQDMECVPCGDPPPPYEPHCTSKVNLVKISSTVSSPRDTALAAVICSALAT
      :::::::::::::::::::::::::::::.::::::::.::.::::::::::::::::::
      FYRKTKLVGFQDMECVPCGDPPPPYEPHCASKVNLVKIASTASSPRDTALAAVICSALAT
              130       140       150       160       170       180

              190       200       210
T127A VLLALLILCVIYCKRQFMEKKPSCKLPSLCLTVKN
      :::::::::::::::::::::::X
      VLLALLILCVIYCKRQFMEKKPSWSLRSQDIQYNGSELSCLDPRQLHEYAHRACCQCRRD
              190       200       210       220       230       240
```

Fig. 15B

```
FASTA searches a protein or DNA sequence data bank
version 2.0u53 July, 1996
Please cite:
W.R. Pearson & D.J. Lipman PNAS (1988) 85:2444-2448

inputs/nb504897.tmp :  981 aa
> Atm472300: 981 aa
vs  library
searching inputs/nb658900.tmp library

  1496 residues in     1 sequences
The best scores are:                                    initn init1 opt
Patent Nucleotide V33362 - (untitled)                    2575 2575 2861

>> Patent Nucleotide V33362 - (untitled)                   (1496 aa)
initn: 2575  init1: 2575  opt: 2861
Smith-Waterman score: 2888;    70.6% identity in 922 aa overlap

               40        50        60        70        80        90
Atm47  CCCCAGCCTCAAACTGCAGTCCGGCGCCGCGGGGCAGGACAAGGGGAAGGAATAAACACG
                                         X:..:. .. :      :. :::::: ::.
                                        GGGAACGTAGAACTCTCCAACAATAAATACA
                                                10        20        30
```

Fig. 16A

```
           100        110        120        130        140        150
Atm47 TTTGGTGAGAGCCATGGCACTCAAGGTCCTACCTCTACACAGGACGGTGCTCTTCGCTGC
      ::::.:.:::.  :::::. : ::.:: :::: . .::: ..:: .. : : :::.::
      TTTGATAAGAAAGATGGCTTTAAAAGTGCTACTAGAACAAGAGAAAACGTTTTTCACTCT
              40        50        60        70        80        90

           160        170        180        190        200        210
Atm47 CATTCTCTTCCTACTCCACCTGGCATGTAAAGTGAGTTGCGAAACCGGAGATTGCAGGCA
       .:. : :: :::   : :   :: ::::::::::: ::: ::::: ::::: :: ::.::
      TTTAGTATTACTAGGCTATTTGTCATGTAAAGTGACTTGTGAAACAGGAGACTGTAGACA
             100       110       120       130       140       150
```

Fig. 16B

```
          220       230       240       250       260       270
Atm47 GCAGGAATTCAAGGATCGATCTGGAAACTGTGTCCTCTGCAAACAGTGCGGACCTGGCAT
      :::.:::::::.::::::.:::::::::::::: : :::::: ::::: ::.::.:::::
      GCAAGAATTCAGGGATCGGTCTGGAAACTGTGTTCCCTGCAACCAGTGTGGGCCAGGCAT
            160       170       180       190       200       210

          280       290       300       310       320       330
Atm47 GGAGTTGTCCAAGGAATGTGGCTTCGGCTATGGGGAGGATGCACAGTGTGTGCCCTGCAG
      ::::::::: :::::::::::::::::::::::::::::::::::::::::: : ::: :
      GGAGTTGTCTAAGGAATGTGGCTTCGGCTATGGGGAGGATGCACAGTGTGTGACGTGCCG
            220       230       240       250       260       270
```

Fig. 16C

```
             340       350       360       370       380       390
Atm47  GCCGCACCGGTTCAAGGAAGACTGGGGTTTCCAGAAGTGTAAGCCATGTGCGGACTGTGC
       :: :::: :::::::::::.:::::::: ::::::::.:: ::::: :::   :::::: ::
       GCTGCACAGGTTCAAGGAGGACTGGGGCTTCCAGAAATGCAAGCCCTGTCTGGACTGCGC
               280       290       300       310       320       330

             400       410       420       430       440       450
Atm47  GCTGGTGAACCGCTTTCAGAGGGCCAACTGCTCACACACCAGTGATGCTGTCTGCGGGGA
       . :::::::::::::::::::.::: :: :: :::  :::::::::::: .::::::::::
       AGTGGTGAACCGCTTTCAGAAGGCAAATTGTTCAGCCACCAGTGATGCCGTCTGCGGGGA
               340       350       360       370       380       390
```

Fig. 16D

```
           460       470       480       490       500       510
Atm47 CTGCCTGCCAGGATTTTACCGGAAGACCAAACTGGTTGGTTTTCAAGACATGGAGTGTGT
      :::: :::::::::::::  ::::::: ::::: :: :: ::::::::::::::::::::
      CTGCTTGCCAGGATTTTATAGGAAGACGAAACTTGTCGGCTTTCAAGACATGGAGTGTGT
             400       410       420       430       440       450

           520       530       540       550       560       570
Atm47 GCCCTGCGGAGACCCACCTCCTCCCTACGAACCACACTGTACCAGCAAGGTGAACCTTGT
      ::: :: ::::::::.:::::::: ::::::::.::::::.:::::::::: ::::: ::
      GCCTTGTGGAGACCCTCCTCCTCCTTACGAACCGCACTGTGCCAGCAAGGTCAACCTCGT
             460       470       480       490       500       510
```

Fig. 16E

```
              580       590       600       610       620       630
Atm47  GAAGATCTCCTCCACCGTCTCCAGCCCTCGGGACACGGCGCTGGCTGCCGTCATCTGCAG
       ::::::: : ::::: : :::::::::.::::::::::::::::::::::: ::::::::
       GAAGATCGCGTCCACGGCCTCCAGCCCACGGGACACGGCGCTGGCTGCCGTTATCTGCAG
                520       530       540       550       560       570

              640       650       660       670       680       690
Atm47  TGCTCTGGCCACGGTGCTGCTCGCCCTGCTCATCCTGTGTGTCATCTACTGCAAGAGGCA
        ::::::::::: :: ::::: :::::::::::::  ::::::::::: :: :::::.::
       CGCTCTGGCCACCGTCCTGCTGGCCCTGCTCATCCCCTGTGTCATCTATTGTAAGAGACA
                580       590       600       610       620       630
```

Fig. 16F

```
            700       710       720       730       740       750
Atm47 GTTCATGGAGAAGAAACCCAGCTGTAAGCTCCCATCCCTCTGTCTCACTGTGAAGTGAGC
      ::: :::::::::::::::::::: .  :: : .:: :.  :.:. .:.::. :. : ::
      GTTTATGGAGAAGAAACCCAGCTGGTCTCTGCGGTCACA-GGACATTCAGTACAACG-GC
              640       650       660       670       680

            760       770       780       790       800       810
Atm47 TTGTTAGCATT-GTCACCCAAGAGTTCTCAAGACACCT-GGCTGAGACCTAAGA-CCTTT
      :  : :::. : :: .:  .: ::.:^:v.  :.::. :.  :..: ::. ::: :::
      TC-TGAGCTGTCGTGTCTTGACAGACCTCAG--CTCCACGAATATGCCCACAGAGCCT--
    690        700       710          720       730       740
```

Fig. 16G

```
             820       830       840       850       860       870
Atm47 AGAGCATCAACAGCTACTTAGAATACAAGATGCAGGAAAACGAGCCTCTTCAGGAATCTC
         ::. : : .:: .:  .::   :. ..:::::.  ..::.:::  : : : .. :::
      ---GCTGCCAGTGCCGCCGTGA---CTCAGTGCAGACCTGCGGGCCGGTGC-GCTTGCTC
            750       760          770       780        790

             880       890       900       910       920       930
Atm47 AGGGCCTCCTAGGGATGCTGGCAAGGCTGTGATGTCTCAAGGCTACCAGGAAAAAATAAA
          : :::..: : :: ::. .::::  :: .: : :::  :  ::.: .: . .:...
      C---CATCCATGTGCTG-TGAGGAGGCC-TGCAGCCCCAA--C--CCGGCGACTCTTGGT
         800       810        820        830           840
```

Fig. 16H

```
          940         950         960         970           980
Atm47 AGTTGTCTATACCCTAAAAAAAAAAAAAAAAAAAAAAAAACATGC--GGCCGC
      .:: :   :. :   ::. :.   :.. .. :.. ::.::: .:: ::   .::::
      TGTGGGGTGCATTCTGCAGCCAGTCTTCAGGCAAGAAACGCAGGCCCAGCCGGGGAGATG
    850        860         870        880         890         900

      GTGCCGACTTTCTTCGGATCCCTCACGCAGTCCATCTGTGGCGAGTTTTCAGATGCCTGG
    910        920         930        940         950         960
```

Fig. 16I

GAATTCGGAACGAGGGGAACCTAATTCTCCTGAGGCTGAGGGAGGGTGGAGGGTCTCAAGGCAACGCTGGCCCCACGAC 79

GGAGTGCCAGGAGCACTAACAGTACCCTTAGCTTGCTTTCCTCCTCCCTCCTTTTTATTTTCAAGTTCCTTTTTATTTC 158

TCCTTGCGTAACAACCTTCTTCCCTTCTGCACCACTGCCCGTACCCTTACCCGCCCCGCCACCTCCTTGCTACCCCACT 237

M P A S S P F L L A P 11
CTTGAAACCACAGCTGTTGGCAGGGTCCCCAGCTC ATG CCA GCC TCA TCT CCT TTC TTG CTA GCC CCC 305

K G P P G N M G G P V R E P A L S V A L 31
AAA GGG CCT CCA GGC AAC ATG GGG GGC CCA GTC AGA GAG CCG GCA CTC TCA GTT GCC CTC 365

W L S W G A A L G A V A C A M A L L T Q 51
TGG TTG AGT TGG GGG GCA GCT CTG GGG GCC GTG GCT TGT GCC ATG GCT CTG CTG ACC CAA 425

Q T E L Q S L R R E V S R L Q G T G G P 71
CAA ACA GAG CTG CAG AGC CTC AGG AGA GAG GTG AGC CGG CTG CAG GGG ACA GGA GGC CCC 485

S Q N G E G Y P W Q S L P E Q S S D A L 91
TCC CAG AAT GGG GAA GGG TAT CCC TGG CAG AGT CTC CCG GAG CAG AGT TCC GAT GCC CTG 545

E A W E N G E R S R K R R A V L T Q K Q 111
GAA GCC TGG GAG AAT GGG GAG AGA TCC CGG AAA AGG AGA GCA GTG CTC ACC CAA AAA CAG 605

K K Q H S V L H L V P I N A T S K D D S 131
AAG AAG CAG CAC TCT GTC CTG CAC CTG GTT CCC ATT AAC GCC ACC TCC AAG GAT GAC TCC 665

D V T E V M W Q P A L R R G R G L Q A Q 151
GAT GTG ACA GAG GTG ATG TGG CAA CCA GCT CTT AGG CGT GGG AGA GGC CTA CAG GCC CAA 725

G Y G V R I Q D A G V Y L L Y S Q V L F 171
GGA TAT GGT GTC CGA ATC CAG GAT GCT GGA GTT TAT CTG CTG TAT AGC CAG GTC CTG TTT 785

Q D V T F T M G Q V V S R E G Q G R Q E 191
CAA GAC GTG ACT TTC ACC ATG GGT CAG GTG GTG TCT CGA GAA GGC CAA GGA AGG CAG GAG 845

T L F R C I R S M P S H P D R A Y N S C 211
ACT CTA TTC CGA TGT ATA AGA AGT ATG CCC TCC CAC CCG GAC CGG GCC TAC AAC AGC TGC 905

Y S A G V F H L H Q G D I L S V I I P R 231
TAT AGC GCA GGT GTC TTC CAT TTA CAC CAA GGG GAT ATT CTG AGT GTC ATA ATT CCC CGG 965

A R A K L N L S P H G T F L G F V K L * 251
GCA AGG GCG AAA CTT AAC CTC TCT CCA CAT GGA ACC TTC CTG GGG TTT GTG AAA CTG TGA 1025

TTGTGTTATAAAAAGTGGCTCCCAGCTTGGAAGACCAGGGTGGGTACATACTGGAGACAGCCAAGAGCTGAGTATATAA 1104

AGGAGAGGGAATGTGCAGGAACAGAGGCATCTTCCTGGGTTTGGCTCCCCGTTCCTCACTTTTCCCTTTTCATTCCCAC 1183

CCCCTAGACTTTGATTTTACGGATATCTTGCTTCTGTTCCCCATGGAGCTCCGAATTCTTGCGTGTGTGTAGATGAGGG 1262

GCGGGGGACGGGCGCCAGGCATTGTTCAGACCTGGTCGGGGCCCACTGGAAGCATCCAGAACAGCACCACCATCTAGCG 1341

GCCGC 1346

Fig. 17

```
T118 pileup.msf  MSF: 286
1913 ..
Name: Trash  Len: 286  Check:  7625  Weight: 1.00
Name: TNF    Len: 286  Check:  5421  Weight: 1.00
Name: tweak  Len: 286  Check:  8867  Weight: 1.00
//
       1                                                          60
TRASH  MPASSPFL...LAPKGPPGNMGGPVREPALSVALWLSWGAALGAVACAMALLTQQTELQS
  TNF  MSTESMIRDVELAEEALPKKTGGP...QGSRRCLFLSLFSFL........IVAGATTLFC
tweak  MAARR........SQRRRGRRGEPGTALLVPLALGLGL.....ALAC.LGLLLAVVSLGS

       61                                                        120
TRASH  LRREVSRLQ.GTGGPSQNGEGYPWQ.SLPEQSSDALEAWENGERSRKRRAVLTQKQKKQH
  TNF  L......LHFGVIGPQR..EEFPRDLSLISPLAQAV.......RSSSRTP.......SDK
tweak  .RASLSAQEPAQEELVAEEDQDPSELNPQTEESQDPAPFLNRLVRPRRSAPKGRKTRARR

       121                                                       180
TRASH  SV.....LHLVPINATSKDDSDVTEVMWQPALRRGRGLQAQGYGVR.....IQDAGVYLL
  TNF  PV.....AHVVANPQAE......GQLQWLN..RRANALLANGVELRDNQLVVPSEGLYLI
tweak  AIAAHYEVHPRPGQDGAQAGVDGTVSGWEEA..RINSSSPLRYNRQIGEFIVTRAGLYYL

       181                                                       240
TRASH  YSQVLFQDVTFTMGQVVSREGQGRQETLFR..............CIRSMPSHPDRA....
  TNF  YSQVLFKGQGCPSTHVLLTHTISRIAVSYQTKVNLL..SAIKSPCQRETPEGAEAK..PW
tweak  YCQVHFDEG................KAVYL.KLDLLVDGVLALRCLEEFSATAASSLGPQ

       241                                          286
TRASH  YNSCYSAGVFHLHQGDILSV.IIPRARAKLNLSPHG.TFLGFVKL.
  TNF  YEPIYLGGVFQLEKGDRLSA.EINRPDY.LDFAESGQVYFGIIAL.
tweak  LRLCQVSGLLALRPGSSLRIRTLPWAHLK...AAPFLTYFGLFQVH
```

Fig. 18

```
GTCGACCCAC GCGTCCGGCA GGATGTTTGC AGTGTCGCGC CCAGGGCTCT GAGACTGAGC      60

CTGCCATCCA CTCGCACGCC TTTCTTTCAG GGCTTTTCGG CTGTTGGCTA CACTGATGTG     120

ACCCCCCTCC CTTTTTGGA ATG ATG GGG ATC TTT TTG GTG TAT GTT GGA TTT     172
                     Met Met Gly Ile Phe Leu Val Tyr Val Gly Phe
                      1               5                   10

GTT TTC TTT TCC GTT TTA TAT GTA CAA CAA GGG CTT TCT TCT CAA GCA      220
Val Phe Phe Ser Val Leu Tyr Val Gln Gln Gly Leu Ser Ser Gln Ala
             15                  20                  25

AAA TTT ACC GAG TTT CCG CGG AAC GTG ACG GCG ACC GAG GGG CAG AAT      268
Lys Phe Thr Glu Phe Pro Arg Asn Val Thr Ala Thr Glu Gly Gln Asn
         30                  35                  40

GTG GAG ATG TCC TGC GCC TTC CAG AGC GGC TCC GCC TCG GTG TAT CTG      316
Val Glu Met Ser Cys Ala Phe Gln Ser Gly Ser Ala Ser Val Tyr Leu
     45                  50                  55

GAG ATC CAA TGG TGG TTC CTG CGG GGG CCG GAG GAC CTG GAT CCC GGG      364
Glu Ile Gln Trp Trp Phe Leu Arg Gly Pro Glu Asp Leu Asp Pro Gly
 60                  65                  70                  75

GCC GAG GGG GCC GGC GCG CAG GTG GAG CTC TTG CCC GAC AGA GAC CCG      412
Ala Glu Gly Ala Gly Ala Gln Val Glu Leu Leu Pro Asp Arg Asp Pro
                 80                  85                  90

GAC AGC GAC GGG ACC AAG ATC AGC ACA GTG AAA GTC CAA GGC AAT GAC      460
Asp Ser Asp Gly Thr Lys Ile Ser Thr Val Lys Val Gln Gly Asn Asp
             95                 100                 105

ATC TCC CAC AAG CTT CAG ATT TCC AAA GTG AGG AAA AAG GAT GAA GGC      508
Ile Ser His Lys Leu Gln Ile Ser Lys Val Arg Lys Lys Asp Glu Gly
        110                 115                 120

TTA TAT GAG TGC AGG GTG ACT GAT GCC AAC TAC GGG GAG CTT CAG GAA      556
Leu Tyr Glu Cys Arg Val Thr Asp Ala Asn Tyr Gly Glu Leu Gln Glu
    125                 130                 135

CAC AAG GCC CAG GCC TAT CTG AAA GTC AAT GCC AAC AGC CAT GCC CGC      604
His Lys Ala Gln Ala Tyr Leu Lys Val Asn Ala Asn Ser His Ala Arg
140                 145                 150                 155

AGA ATG CAG GCC TTC GAA GCC TCG CCC ATG TGG CTG CAG GAT ATG AAG      652
Arg Met Gln Ala Phe Glu Ala Ser Pro Met Trp Leu Gln Asp Met Lys
                160                 165                 170

CCC CGC AAG AAC GTC TCC GCA GCC ATC CCC AGC AGC ATC CAT GGC TCT      700
Pro Arg Lys Asn Val Ser Ala Ala Ile Pro Ser Ser Ile His Gly Ser
            175                 180                 185

GCC AAC CAA CGA ACG CAC TCC ACC TCC AGC CCT CAA GTG GTA GCC AAA      748
Ala Asn Gln Arg Thr His Ser Thr Ser Ser Pro Gln Val Val Ala Lys
        190                 195                 200
```

Fig. 19A

```
ATC CCC AAA CAA AGT CCA CAA TCA GGT ATG GAA ACC CAT TTC GAG CCT    796
Ile Pro Lys Gln Ser Pro Gln Ser Gly Met Glu Thr His Phe Glu Pro
    205                 210                 215

TTT ATT TTA CCA CTC ACA AAC GCT CCA CAG AAA GGT CAG TCG TAT AGA    844
Phe Ile Leu Pro Leu Thr Asn Ala Pro Gln Lys Gly Gln Ser Tyr Arg
220                 225                 230                 235

GTA GAC AGA TTT ATG AAT GGT GAT TTT TAAAATCGGA GACCTAGTTC          891
Val Asp Arg Phe Met Asn Gly Asp Phe
                240

AGTGCAAGTG ATTATGAGAG GTGAGCACTG AGCCTGCACC AATTCACTCA GAGCTCAAAG  951

CATGTGGGTG CACCCCGTCA GTCCCCTAGT GGTGCTTCAT TTCCAGGGCA TCTGAGAGCT 1011

GGACTCTGGT TTTTATCCTT TCTGTATTTA CACATTATAA GAACAATAAA TCATGTAATG 1071

TTGGTTACAT TACAAAAAAA AAAAAAAAAA AAAAAAAAGG GCGGCCGC              1119
```

Fig. 19B

```
CACGCGTCCG CAGCCAGCCG GCGGCGGAGA CACTTCACGG CGTGGCAACC CGGGTCTGTG    60

CCTTGAAGCC TCCGGATCGC AGCCAGCTCG GTCCATCCCT CACTAGTCGC AATCCCCTGT   120

GTCCAAGCTA CTCTTTGCTA TGAGCGGCAG CATGCGTGCA GTATCGCGCC CCAGGCTCTG   180

AGAGCAGCCT GCGGACACGC TTGCCTATCT GTCTTTTTAG GTTTTGGGGC TCTGGGCTAC   240

ACGGATGTGC CCCACTCCCT TGGCATG ATG GGG ATC TTT TTG GCG TCT GTT       291
                              Met Gly Ile Phe Leu Ala Ser Val
                               1               5

GGA TTT ATG TTC TTT TCC GTG TTA TAT GTA CAA CAA GGG CTT TCT TCT     339
Gly Phe Met Phe Phe Ser Val Leu Tyr Val Gln Gln Gly Leu Ser Ser
    10                  15                  20

CAA GCA AAA TTT ACC GAG TTG CCG AGA AAT GTG ACT GCT ACC GAA GGG     387
Gln Ala Lys Phe Thr Glu Leu Pro Arg Asn Val Thr Ala Thr Glu Gly
 25                  30                  35                  40

CAA AAT GTG GAG ATG TCC TGT GCT TTC CAA AGC GGC TCT GCT TCA GTG     435
Gln Asn Val Glu Met Ser Cys Ala Phe Gln Ser Gly Ser Ala Ser Val
                 45                  50                  55

TAC CTG GAG ATC CAG TGG TGG TTC CTT CGG GGG CCA GAG GAC CTG GAG     483
Tyr Leu Glu Ile Gln Trp Trp Phe Leu Arg Gly Pro Glu Asp Leu Glu
             60                  65                  70

CAA GGC ACG GAG GCT GCA GGC TCG CAG GTG GAG CTC TTA CCC GAC AGA     531
Gln Gly Thr Glu Ala Ala Gly Ser Gln Val Glu Leu Leu Pro Asp Arg
         75                  80                  85

GAC CCG GAC AAC GAT GGG ACC AAG ATT AGT ACA GTG AAA GTC CAA GGC     579
Asp Pro Asp Asn Asp Gly Thr Lys Ile Ser Thr Val Lys Val Gln Gly
    90                  95                  100

AAT GAT ATC TCC CAC AAG CTT CAG ATA TCC AAA GTG AGA AAA AAG GAT     627
Asn Asp Ile Ser His Lys Leu Gln Ile Ser Lys Val Arg Lys Lys Asp
105                 110                 115                 120

GAA GGT TTA TAC GAG TGC AGG GTG ACT GAC GCT AAC TAC GGG GAG CTT     675
Glu Gly Leu Tyr Glu Cys Arg Val Thr Asp Ala Asn Tyr Gly Glu Leu
                125                 130                 135

CAG GAA CAC AAG GCC CAG GCC TAT CTG AAA GTC AAT GCC AAC AGC CAT     723
Gln Glu His Lys Ala Gln Ala Tyr Leu Lys Val Asn Ala Asn Ser His
            140                 145                 150

GCT CGG AGG ATG CAG GCC TTT GAA GCC TCA CCT ATG TGG CTG CAA GAC     771
Ala Arg Arg Met Gln Ala Phe Glu Ala Ser Pro Met Trp Leu Gln Asp
        155                 160                 165

ACG AAG CCT CGA AAG AAC GCA TCA TCG GTG GTT CCC AGC AGC GTC CAC     819
Thr Lys Pro Arg Lys Asn Ala Ser Ser Val Val Pro Ser Ser Val His
    170                 175                 180
```

Fig. 20A

```
AAC TCT GCC AAC CAA CGA ATG CAC TCC ACC TCC AGC CCT CAA GCG GTA      867
Asn Ser Ala Asn Gln Arg Met His Ser Thr Ser Ser Pro Gln Ala Val
185                 190                 195                 200

GCC AAA ATC CCC AAG CAA AGT CCA CAA TCA GCA AAG AGC AAA TCG CCT      915
Ala Lys Ile Pro Lys Gln Ser Pro Gln Ser Ala Lys Ser Lys Ser Pro
            205                 210                 215

GTA AAA TCT ACG GAG CGG ACA GCA AAG TTG ACC CTA TAC TCC AAG CAC      963
Val Lys Ser Thr Glu Arg Thr Ala Lys Leu Thr Leu Tyr Ser Lys His
        220                 225                 230

CAT TCT GCA CCC CTG TAC TCT AGT TAT CTA CAC AAG GAG CAT CAG CTT     1011
His Ser Ala Pro Leu Tyr Ser Ser Tyr Leu His Lys Glu His Gln Leu
    235                 240                 245

CCG GAA GCA TAAGTGAAGA CACTGTCACA CGCTTTATTG ATAATATTTT             1060
Pro Glu Ala
    250

CTTTGGGAAG TTGCTGATCT TTTATTTCAA GAGAATTAAT GGGAAGAGAT AGGACATTTT  1120
CCAATTACAA GACCAATTTT TTTCCTTTTA TTTCAACAAA TAAAACCTGC ATTTCACTGA  1180
CTGCTCAGGA GTTGGCCTGA ATGACATCAG TATACTAAAT ATTTCCATGG ATTCCACCAA  1240
TTTCCTAACG AGGGACACCT AATCTTCAAG AAGCAAACAA AGATGGAAAA CCTAAGAACC  1300
ACAAACTGTC TCATACAGCA CCCCAGCTGA GGAACAAAAC AAATAGCTAA ATGCTGACCA  1360
TGGCAAATCA ACATCAGACA ACTTTATTTT ACATATGGAA TAATCAAAGA AAGTTTTTTT  1420
TTTACTTCCT TTTTGCCCCC TGGAATTTAT CTTGGAGTTT CCCTTTTTTC CTTGATTGCC  1480
GTTTTCGTTC AATGGTAGCA AGTGCCAATT ATGGCCAATC CTTGTCAATC CTGGAAGGTT  1540
TATATTCATA TACATTGAGT GTGGTATATA TCAATGTATT TTAATTCATT TGGCAATTTC  1600
TGTATAGGCA AACCTGGCAA ATTCTGTAAA TTGCTTATAG TATGTGTGAT ATGACTTCAA  1660
GGTAGATAGG CTATGATGCT CATGCAAGCT GACTTTCTTC ATTCTATATA CAAATATATT  1720
CATGAGCATA TATTAGGCCA CCAACTTCTT TTCCTAAAGA ATTATTTTTC ATTTGTACCT  1780
CATGTATTTT GTGAATTTTG TAGTATATTT CTCTGTTCCA CTAGTTTGAC CGCTACAGTT  1840
TGTCTCTGTT GTCCTCTACT TCCTTCTGGA AAAATTTAAA ATTGTGTATG TCTCTGATAA  1900
ATGAATTAAT TTTGTTGTGT GTATGCTATG TTGGAATTTG CTGTGTTCTT TTAAACATGT  1960
ATTTATTAAG GTTTGGGGAT CTTGAGTTGA GTCTGAAGAA TGCACACCTG GTTTTTGACA  2020
GAGTTCCTCA TGTTACCAAT ATTCTATCTC AGAGAAAGAA AGACACCAAG TGGGAAAACT  2080
AAGAAGACAT TTTGACTTCC CAAGATCCTG GAAGAGCACT TCACACTCTG ACTAAATAAT  2140
GTTGCTTTTT TTGTTCTTCA AGACTTTTTT GTAGCTTTGT CTTTCTGTTA GTTGCTGCTA  2200
ATTATATTTT AATGTCTACT AATTAAAAAT TAAAATGTGA TTGTTGGCTG AATACAATAT  2260
```

Fig. 20B

GCAAATGACT GCAAAGCCCA TACTGAAGAA AATAGATGTT TAATCTTCAC TCAATAATTA 2320

TAATTTTAAA TAGTTCATCA TTATTTTTTG ACCTTATGAT ATTTTGTTTA GACCTGTTCT 2380

AATTACATCT TTCTCTGGCA AAGAAAGATA GAACAATCAA TACATTCCCT CTTACAGTAT 2440

GGAATGGTTG TGGCTTAAGA AAGAATGCAT CCAGATGGTC TTCCAGAGAG ATTATTTTAT 2500

TTTCATTATA AAACCAGAAA CCATATATGT AGGAATGGTT CATTCCTAAT GTAAGGCCAT 2560

AAATTGTAGC TTGAAGGCAA GGAATACATT TGTTTTTTTA TGGTAAAGGA CTGGCCTCTG 2620

ACATGCACTT ATAAGCAATG TGAATATTTT CATAATATGC TTGACATTCT CCTTTAACAA 2680

ATATTGTTTT ATGGTAAATC TTTCCTTGCC ATTTTTCTTC TTTCATTTGA TTCATTATTT 2740

CATTCTAATG AAGAAAATAA AGGTTTAATT ATGATACTTT ATTAACATAC AAATGTATTT 2800

TCTTTCTAAG TTAAATATCT GAAAGTTGTA TAAAATGATG GTAGAGAAAT ATTACTCATT 2860

CGGTTTCTTT GAGCTTTAAG AATCCCATAC ATTGCAGTAT ATATTAGAAT ACTGATTTAA 2920

CATCAAACTG GGGGGGAAAA TCATGTATTA TACTTTTACT CAATGTCTAG GTAATGGATT 2980

CAGCTAATTT TACAGCAAGC CAAATGTGTA CCCGTATCAG TAATGTTCAC CATGCTTGTA 3040

ATAAAAGGGC ATATGCTAGT TTTGGAAGAA TGCTCATTAG ATTCATTGTA TCAGTGTCCA 3100

AAATAATAAA GACCTGTTTA TCACTGTGAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 3160

AAAAAAAAAA AAAAAAAAAA AAAAAAGGGC GGCCGC 3196

Fig. 20C

```
>_ hT122                                         244 aa vs.
>_ mT122                                         251 aa
scoring matrix: , gap penalties: -12/-2
77.4% identity;         Global alignment score: 1236

                  10        20        30        40       *50        60
hT122     MMGIFLVYVGFVFFSVLYVQQGLSSQAKFTEFPRNVTATEGQNVEMSCAFQSGSASVYLE
          : ::::. :::.::::::::::::::::::.:::::::::::::::::::::::::::::
mT122     M-GIFLASVGFMFFSVLYVQQGLSSQAKFTELPRNVTATEGQNVEMSCAFQSGSASVYLE
                   10        20        30        40      * 50

                  70        80        90       100       110       120
hT122     IQWWFLRGPEDLDPGAEGAGAQVELLPDRDPDSDGTKISTVKVQGNDISHKLQISKVRKK
          ::::::::::::. :.:.::.:::::::::::.:::::::::::::::::::::::::::
mT122     IQWWFLRGPEDLEQGTEAAGSQVELLPDRDPDNDGTKISTVKVQGNDISHKLQISKVRKK
         60        70        80        90       100       110

                *130       140       150       160       170       180
hT122     DEGLYECRVTDANYGELQEHKAQAYLKVNANSHARRMQAFEASPMWLQDMKPRKNVSAAI
          ::::::::::::::::::::::::::::::::::::::::::::::::: :::::.:...
mT122     DEGLYECRVTDANYGELQEHKAQAYLKVNANSHARRMQAFEASPMWLQDTKPRKNASSVV
        120     * 130       140       150       160       170

                 190       200       210             220       230
hT122     PSSIHGSANQRTHSTSSPQVVAKIPKQSPQSG-----METHFEPFILPLTNAPQKG---Q
          :::.:.::::: :::::::.:::::::::::.      ... .   : :. ...     .
mT122     PSSVHNSANQRMHSTSSPQAVAKIPKQSPQSAKSKSPVKSTERTAKLTLYSKHHSAPLYS
        180       190       200       210       220       230

               240
hT122     SYRVDRFMNGDF
          ::   . .  .
mT122     SYLHKEHQLPEA
        240       250

Elapsed time:    0:00:00
```

Fig. 21

GTCGACCCACGCGTCCGGAGCCCGGGGCGGGTGGACGCGGACTCGAACGCAGTTGCTTCGGGACCCAGGACCCCCTCGG 79

GCCCGACCCGCCAGGAAAGACTGAGGCCGCGGCCTGCCCCGCCCGGCTCCCTGCGCCGCCGCCGCCTCCCGGACAGAA 158

M C S R V P L L L P L L L L L A L G P 19
G ATG TGC TCC AGG GTC CCT CTG CTG CTG CCG CTG CTC CTG CTA CTG GCC CTG GGG CCT 216

G V Q G C P S G C Q C S Q P Q T V F C T 39
GGG GTG CAG GGC TGC CCA TCC GGC TGC CAG TGC AGC CAG CCA CAG ACA GTC TTC TGC ACT 276

A R Q G T T V P R D V P P D T V G L Y V 59
GCC CGC CAG GGG ACC ACG GTG CCC CGA GAC GTG CCA CCC GAC ACG GTG GGG CTG TAC GTC 336

F E N G I T M L D A G S F A G L P G L Q 79
TTT GAG AAC GGC ATC ACC ATG CTC GAC GCA GGC AGC TTT GCC GGC CTG CCG GGC CTG CAG 396

L L D L S Q N Q I A S L P S G V F Q P L 99
CTC CTG GAC CTG TCA CAG AAC CAG ATC GCC AGC CTG CCC AGC GGG GTC TTC CAG CCA CTC 456

A N L S N L D L T A N R L H E I T N E T 119
GCC AAC CTC AGC AAC CTG GAC CTG ACG GCC AAC AGG CTG CAT GAA ATC ACC AAT GAG ACC 516

F R G L R R L E R L Y L G K N R I R H I 139
TTC CGT GGC CTG CGG CGC CTC GAG CGC CTC TAC CTG GGC AAG AAC CGC ATC CGC CAC ATC 576

Fig. 22A

Q P G A F D T L D R L L E L K L Q D N E 159
CAG CCT GGT GCC TTC GAC ACG CTC GAC CGC CTC CTG GAG CTC AAG CTG CAG GAC AAC GAG 636

L R A L P P L R L P R L L L L D L S H N 179
CTG CGG GCA CTG CCC CCG CTG CGC CTG CCC CGC CTG CTG CTG CTG GAC CTC AGC CAC AAC 696

S L L A L E P G I L D T A N V E A L R L 199
AGC CTC CTG GCC CTG GAG CCC GGC ATC CTG GAC ACT GCC AAC GTG GAG GCG CTG CGG CTG 756

A G L G L Q Q L D E G L F S R L R N L H 219
GCT GGT CTG GGG CTG CAG CAG CTG GAC GAG GGG CTC TTC AGC CGC TTG CGC AAC CTC CAC 816

D L D V S D N Q L E R V P P V I R G L R 239
GAC CTG GAT GTG TCC GAC AAC CAG CTG GAG CGA GTG CCA CCT GTG ATC CGA GGC CTC CGG 876

G L T R L R L A G N T R I A Q L R P E D 259
GGC CTG ACG CGC CTG CGG CTG GCC GGC AAC ACC CGC ATT GCC CAG CTG CGG CCC GAG GAC 936

L A G L A A L Q E L D V S N L S L Q A L 279
CTG GCC GGC CTG GCT GCC CTG CAG GAG CTG GAT GTG AGC AAC CTA AGC CTG CAG GCC CTG 996

P G D L S G L F P R L R L L A A A R N P 299
CCT GGC GAC CTC TCG GGC CTC TTC CCC CGC CTG CGG CTG CTG GCA GCT GCC CGC AAC CCC 1056

F N C V C P L S W F G P W V R E S H V T 319
TTC AAC TGC GTG TGC CCC CTG AGC TGG TTT GGC CCC TGG GTG CGC GAG AGC CAC GTC ACA 1116

Fig. 22B

L A S P E E T R C H F P P K N A G R L L 339
CTG GCC AGC CCT GAG GAG ACG CGC TGC CAC TTC CCG CCC AAG AAC GCT GGC CGG CTG CTC 1176

L E L D Y A D F G C P A T T T T A T V P 359
CTG GAG CTT GAC TAC GCC GAC TTT GGC TGC CCA GCC ACC ACC ACC ACA GCC ACA GTG CCC 1236

T T R P V V R E P T A L S S S L A P T W 379
ACC ACG AGG CCC GTG GTG CGG GAG CCC ACA GCC TTG TCT TCT AGC TTG GCT CCT ACC TGG 1296

L S P T A P A T E A P S P P S T A P P T 399
CTT AGC CCC ACA GCG CCG GCC ACT GAG GCC CCC AGC CCG CCC TCC ACT GCC CCA CCG ACT 1356

V G P V P Q P Q D C P P S T C L N G G T 419
GTA GGG CCT GTC CCC CAG CCC CAG GAC TGC CCA CCG TCC ACC TGC CTC AAT GGG GGC ACA 1416

C H L G T R H H L A C L C P E G F T G L 439
TGC CAC CTG GGG ACA CGG CAC CAC CTG GCG TGC TTG TGC CCC GAA GGC TTC ACG GGC CTG 1476

Y C E S Q M G Q G T R P S P T P V T P R 459
TAC TGT GAG AGC CAG ATG GGG CAG GGG ACA CGG CCC AGC CCT ACA CCA GTC ACG CCG AGG 1536

P P R S L T L G I E P V S P T S L R V G 479
CCA CCA CGG TCC CTG ACC CTG GGC ATC GAG CCG GTG AGC CCC ACC TCC CTG CGC GTG GGG 1596

L Q R Y L Q G S S V Q L R S L R L T Y R 499
CTG CAG CGC TAC CTC CAG GGG AGC TCC GTG CAG CTC AGG AGC CTC CGT CTC ACC TAT CGC 1656

Fig. 22C

N L S G P D K R L V T L R L P A S L A E 519
AAC CTA TCG GGC CCT GAT AAG CGG CTG GTG ACG CTG CGA CTG CCT GCC TCG CTC GCT GAG 1716

Y T V T Q L R P N A T Y S V C V M P L G 539
TAC ACG GTC ACC CAG CTG CGG CCC AAC GCC ACT TAC TCC GTC TGT GTC ATG CCT TTG GGG 1776

P G R V P E G E E A C G E A H T P P A V 559
CCC GGG CGG GTG CCG GAG GGC GAG GAG GCC TGC GGG GAG GCC CAT ACA CCC CCA GCC GTC 1836

H S N H A P V T Q A R E G N L P L L I A 579
CAC TCC AAC CAC GCC CCA GTC ACC CAG GCC CGC GAG GGC AAC CTG CCG CTC CTC ATT GCG 1896

P A L A A V L L A A L A A V G A A Y C V 599
CCC GCC CTG GCC GCG GTG CTC CTG GCC GCG CTG GCT GCG GTG GGG GCA GCC TAC TGT GTG 1956

R R G R A M A A A A Q D K G Q V G P G A 619
CGG CGG GGG CGG GCC ATG GCA GCA GCG GCT CAG GAC AAA GGG CAG GTG GGG CCA GGG GCT 2016

G P L E L E G V K V P L E P G P K A T E 639
GGG CCC CTG GAA CTG GAG GGA GTG AAG GTC CCC TTG GAG CCA GGC CCG AAG GCA ACA GAG 2076

G G G E A L P S G S E C E V P L M G F P 659
GGC GGT GGA GAG GCC CTG CCC AGC GGG TCT GAG TGT GAG GTG CCA CTC ATG GGC TTC CCA 2136

G P G L Q S P L H A K P Y I * 674
GGG CCT GGC CTC CAG TCA CCC CTC CAC GCA AAG CCC TAC ATC TAA 2181

Fig. 22D

GCCAGAGAGAGACAGGGCAGCTGGGGCCGGGCTCTCAGCCAGTGAGATGGCCAGCCCCCTCCTGCTGCCACACCACGTA 2260

AGTTCTCAGTCCCAACCTCGGGGATGTGTGCAGACAGGGCTGTGTGACCACAGCTGGGCCCTGTTCCCTCTGGACCTCG 2339

GTCTCCTCATCTGTGAGATGCTGTGGCCCAGCTGACGAGCCCTAACGTCCCCAGAACCGAGTGCCTATGAGGACAGTGT 2418

CCGCCCTGCCCTCCGCAACGTGCAGTCCCTGGGCACGGCGGGCCCTGCCATGTGCTGGTAACGCATGCCTGGGCCCTGC 2497

TGGGCTCTCCCACTCCAGGCGGACCCTGGGGGCCAGTGAAGGAAGCTCCCGGAAAGAGCAGAGGGAGAGCGGGTAGGCG 2576

GCTGTGTGACTCTAGTCTTGGCCCCAGGAAGCGAAGGAACAAAAGAAACTGGAAAGGAAGATGCTTTAGGAACATGTTT 2655

TGCTTTTTTAAAATATATATATATATTTATAAGAGATCCTTTCCCATTTATTCTGGAAGATGTTTTTCAAACTCAGAGAC 2734

AAGGACTTTGGTTTTTGTAAGACAAACGATGATATGAAGGCCTTTTGTAAGAAAAAATAAAAGATGAAGTGTGAAAAAA 2813

AAAAAAAAAAAAAAAAAAAAAAAAAAAAAGGGCGGCCGC 2852

Fig. 22E

```
          1                                                          60
LRSG-1    MCSRVPLLLPLLLLL---ALGP-GVQG------------CPSGCQCS-----QPQTVFC
GPV       M-LRGTLLCAVLGLLR------------------AQPFPCPPACKCVFRDAAQ-----C
IGFBP     MALRKGGLALALLLLSWVALGPRSLEGAEPGTPGEAEGPACPATCACSYDDEVNELSVFC

          61                                                        120
LRSG-1    TARQGTTVPR-DVPPDTVGLYVFENGITMLDAGSFAGLPGLQLLDLSQNQIASLPSGVFQ
GPV       SGGDVARISALGLP----------------------TNLTHILLFGMGRGVLQSQSFS
IGFBP     SSRNLTRLPD-GIPGGTQALWLDSNNLSSIPPAAFRNLSSLAFLNLQGGQLGSLEPQALL

          121                                                       180
LRSG-1    PLANLSNLDLTANRLHEITNETFRGLRRLERLYLGKNRIRHIQPGAFDTLDRLLELKLQD
GPV       GMTVLQRLMISDSHISAVAPGTFSDLIKLKTLRLSRNKITHLPGALLDKMVLLEQLFLDH
IGFBP     GLENLCHLHLERNQLRSLAVGTFAYTPALALLGLSNNRLSRLEDGLFEGLGNLWDLNLGW

          181                                                       240
LRSG-1    NELRALPPLRLPRLLLLD---LSHNSLLALEPGILDT-ANVEALRLAGLGLQQLDEGLFS
GPV       NALRGIDQNMFQKLVNLQELALNQNQLDFLPASLFTNLENLKLLDLSGNNLTHLPKGLLG
IGFBP     NSLAVLPDAAFRGLGGLRELVLAGNRLAYLQPALFSGLAELRELDLSRNALRAIKANVFA

          241                                                       300
LRSG-1    RLRNLHDLDVSDNQLERVPP-VIRGLRGLTRLRLAGNTRIAQLRPEDLAGLAALQELDVS
GPV       AQAKLERLLLHSNRLVSLDSGLLNSLGALTELQFH-RNHIRSIAPGAFDRLPNLSSLTLS
IGFBP     QLPRLQKLYLDRNLIAAVAPGAFLGLKALRWLDLS-HNRVAGLLEDTFPGLLGLRVLRLS

          301                                                       360
LRSG-1    NLSLQALPGDLSGLFPRLRLLAAARNPFNCVCPLSWFGPWVRESHVTLASPEETRCHFPP
GPV       RNHLAFLPSALFLHSHNLTLLTLFENPLAEL-PGVLFGEMGGLQELWL-----NRTQL--
IGFBP     HNAIASLRPRTFEDLHFLEELQLGHNRIRQL-AERSFEGLGQLEVLTL-----DHNQLQE
```

Fig. 23A

	361 ... 420
LRSG-1	KNAGRLL--LELDYADFG--CPATTTTATVPTTRPVVREPTALSSSLAPTWLSPTA-PAT
GPV	---------------------*RTLPAAAFRNLSRLRYLGVTLSPRLSA*--*LPQGAFQGL*
IGFBP	*VKVGAFLGLTNVAVMNLSGNCLRNLPEQVFRGLGKLHSLHLE*-*GSCLGR*--*IRPHTFAGL*

	421 ... 480
	* * * * * *
LRSG-1	EAPSPPSTAPPTVGPVPQPQDCPPSTCLNGGTCHLG---TRHHLACLCPEGFTGLYCES-
GPV	*GELQVLALHSNGLTALPDGL*-------*LRGLGKLRQVSLRRNRLRALPRALFRNLSSLES*
IGFBP	*SGLRRLFLKDNGLVGIEEQS*-------*LWGLAELLELDLTSNQLTHLPHQLFQGLGKLEY*

	481 ... 540
LRSG-1	-QMGQGTRPS-PTPVTPR**PPRSLTLGIEPVSPTSLRVGLQRYLQGSSVQLRSLRLTYRNL**
GPV	*VQLDHNQLETLPGDVFGALPRLTE*VLLGHNSWRCDCG-LGPFLG-------WLR-QHLGL
IGFBP	*LLLSHNRLAELPADALGPLQRAFWLDVSHNRLEALPGSLLASLG*-------*RLR*--*YLNL*

	541 ... 600
LRSG-1	**SGPDKRLVTLRLPASLAEYTVTQLRPNATYSVCV**MPLGPGRVPEGEEACGEAHTPPAVHS
GPV	VGGEEPPRCAG-PGAHAGLPLWALPGGD--AECPGPRGPPPRPAADSSSEAPVHPALAPN
IGFBP	R--*NNSLRTFT*-*PQPPGLERLW*-*LEGNP*--WDCSCPLKALRDFALQNPSAVPR-------

	601 ... 660
LRSG-1	NHAP------VTQAREGNLPLLIAPALAAVLLAALAAVGAAYCVRRGRAMAAAAQDKGQV
GPV	SSEPWVWAQPVTTGKGQDHSPFWGFYFLLLAVQAMITVIIVFAMIK--------------
IGFBP	------FVQAICEG-DDCQPPVYTYNNITCASPPEVAGLDL-------------------

	661 ... 718
LRSG-1	GPGAGPLELEGVKVPLEPGPKATEGGGEALPSGSECEVPLMGFPGPGLQSPLHAKPYI
GPV	---IGQLFRKLIRER-ALG---------------------------------------
IGFBP	--------RDLGEAHFAPC---------------------------------------

Fig. 23B

```
GTCGACCCACGCGTCCGGGAGCCGGAGCCAGAGACCGGGGCTGGGAAACCCCAGCCCGGGACGGGACGCAGCAGCCTCT   79

GGATCCCGGGACCCCGGACCTCTCAGGACCGGCCAGAGGTGAAGGACTGAGGCCCCACTGAGGCCTTGGACCGCACCGC  158

                                     M   H   S   R   S   C   L   P   P   L        10
CTGGCTCCTTCAGCCGCAGTCGTCTCCTGGGACAGAAG ATG CAC TCC AGG AGC TGC CTG CCA CCT CTC   226

 L   L   L   L   L   V   L   L   G   S   G   V   Q   G   C   P   S   G   C   Q    30
CTG TTG TTG CTT CTG GTG CTC CTG GGG TCT GGA GTA CAG GGT TGC CCA TCA GGC TGC CAG  286

 C   N   Q   P   Q   T   V   F   C   T   A   R   Q   G   T   T   V   P   R   D    50
TGC AAC CAG CCA CAG ACA GTC TTC TGC ACT GCC CGT CAG GGA ACC ACA GTG CCC CGA GAC  346

 V   P   P   D   T   V   G   L   Y   I   F   E   N   G   I   T   T   L   D   V    70
GTG CCA CCT GAC ACA GTG GGC CTG TAC ATC TTT GAG AAC GGC ATC ACG ACA CTT GAT GTG  406

 G   C   F   A   G   L   P   G   L   Q   L   L   D   L   S   Q   N   Q   I   T    90
GGC TGT TTT GCT GGC CTT CCG GGC CTG CAG CTT CTG GAC TTG TCA CAG AAC CAG ATC ACT  466

 S   L   P   G   G   I   F   Q   P   L   V   N   L   S   N   L   D   L   T   A   110
AGC CTG CCC GGG GGC ATC TTT CAG CCA CTT GTT AAC CTC AGT AAC CTG GAC CTG ACT GCC  526

 N   K   L   H   E   I   S   N   E   T   F   R   G   L   R   R   L   E   R   L   130
AAC AAA CTG CAC GAG ATC TCC AAC GAG ACC TTC CGT GGC CTG CGG CGC CTG GAG CGC CTC  586

 Y   L   G   K   N   R   I   R   H   I   Q   P   G   A   F   D   A   L   D   R   150
TAC CTG GGC AAG AAC CGA ATT CGC CAC ATC CAA CCG GGT GCC TTC GAC GCG CTT GAT CGC  646
```

Fig. 24A

L L E L K L P D N E L R V L P P L H L P 170
CTC CTG GAG CTC AAG CTG CCA GAC AAT GAG CTT CGG GTG TTG CCC CCA TTG CAC TTG CCC 706

R L L L L D L S H N S I P A L E A G I L 190
CGC CTG CTG CTG CTT GAC CTC AGC CAC AAC AGC ATC CCA GCC CTG GAA GCC GGA ATA CTG 766

D T A N V E A L R L A G L G L R Q L D E 210
GAT ACC GCC AAT GTA GAG GCA TTG AGG TTG GCT GGC CTA GGG CTG CGG CAG CTG GAT GAG 826

G L F G R L L N L H D L D V S D N Q L E 230
GGG CTT TTT GGC CGC CTT CTC AAC CTC CAT GAC TTG GAT GTT TCT GAC AAC CAG TTG GAG 886

H M P S V I Q G L R G L T R L R L A G N 250
CAT ATG CCA TCT GTG ATT CAA GGC CTG CGT GGC CTG ACA CGC CTG CGG CTG GCT GGC AAC 946

T R I A Q I R P E D L A G L T A L Q E L 270
ACC CGT ATT GCC CAG ATA CGG CCC GAG GAC CTC GCT GGT CTG ACT GCC CTA CAG GAA TTG 1006

D V S N L S L Q A L P S D L S S L F P R 290
GAT GTG AGC AAC CTA AGC CTG CAG GCC CTG CCC AGT GAC CTC TCG AGT CTC TTT CCC CGC 1066

L R L L A A A R N P F N C L C P L S W F 310
CTG CGC CTC TTA GCA GCT GCC AGG AAC CCC TTC AAC TGC TTG TGC CCC TTG AGC TGG TTT 1126

G P W V R E N H V V L A S P E E T R C H 330
GGT CCT TGG GTG CGT GAG AAC CAT GTT GTG TTG GCC AGC CCT GAG GAG ACG CGT TGT CAC 1186

Fig. 24B

F P P K N A G R L L L D L D Y A D F G C 350
TTT CCA CCC AAG AAT GCT GGC CGA CTG CTC CTG GAT CTG GAT TAT GCA GAT TTT GGC TGC 1246

P V T T T T A T V P T I R S T I R E P T 370
CCA GTC ACC ACT ACC ACG GCC ACA GTA CCT ACT ATA AGG TCT ACT ATC AGG GAA CCC ACA 1306

L S T S S Q A P T W P S L T E P T T Q A 390
CTT TCA ACT TCT AGC CAA GCT CCC ACC TGG CCC AGC CTC ACA GAG CCA ACT ACC CAG GCC 1366

S T V L S T A P P T M R P A P Q P Q D C 410
TCC ACC GTA CTA TCG ACT GCC CCA CCA ACC ATG AGG CCA GCT CCT CAG CCC CAG GAC TGT 1426

P A S I C L N G G S C R L G A R H H W E 430
CCA GCA TCC ATC TGC CTG AAT GGT GGT AGC TGC CGT TTG GGA GCA AGA CAC CAC TGG GAG 1486

C L C P E G F I G L Y C E S P V E Q G M 450
TGC CTA TGC CCT GAG GGC TTC ATT GGC CTG TAC TGT GAG AGT CCA GTG GAG CAA GGG ATG 1546

K P S S I P D T P R P P P L L P L S I E 470
AAG CCC AGC TCC ATA CCA GAC ACT CCA AGG CCC CCT CCA CTG CTG CCT CTC AGC ATT GAG 1606

P V S P T S L R V K L Q R Y L Q G N T V 490
CCG GTG AGC CCC ACC TCC TTG CGT GTG AAG CTG CAG CGC TAC TTG CAG GGT AAC ACT GTG 1666

Q L R S L R L T Y R N L S G P D K R L V 510
CAG CTA CGG AGC CTC CGG CTC ACC TAT CGC AAC CTG TCT GGC CCT GAC AAA CGA CTG GTG 1726

Fig. 24C

T L R L P A S L A E Y T V T Q L R P N A 530
ACA TTA CGG CTG CCT GCT TCA CTT GCA GAG TAT ACA GTC ACC CAG CTG CGA CCC AAT GCC 1786

T Y S I C V T P L G A G R T P E G E E A 550
ACC TAT TCT ATC TGT GTC ACA CCC TTG GGA GCT GGA CGG ACA CCT GAA GGT GAG GAG GCC 1846

C G E A N T S Q A V R S N H A P V T Q A 570
TGT GGG GAG GCC AAC ACT TCC CAG GCA GTC CGC TCT AAC CAT GCC CCA GTT ACC CAG GCC 1906

R E G N L P L L I A P A L A A V L L A V 590
CGT GAG GGC AAC CTG CCA CTC CTC ATT GCG CCT GCC CTG GCT GCT GTA CTT CTG GCT GTG 1966

L A A A G A A Y C V R R A R A T S T A Q 610
TTA GCC GCT GCA GGG GCA GCC TAC TGT GTG CGG CGG GCA CGG GCA ACT TCT ACA GCT CAG 2026

D K G Q V G P G T G P L E L E G V K A P 630
GAC AAA GGG CAG GTG GGG CCA GGG ACT GGA CCC CTG GAA CTA GAG GGG GTG AAA GCC CCT 2086

L E P G S K A T E G G G E A L S G G P E 650
TTG GAG CCA GGC TCC AAG GCA ACA GAG GGA GGT GGG GAG GCT TTG TCA GGT GGT CCT GAA 2146

C E V P L M G Y P G P S L Q G V L P A K 670
TGT GAG GTG CCT CTT ATG GGC TAC CCA GGG CCC AGC CTT CAG GGG GTC CTC CCT GCT AAG 2206

H Y I * 674
CAC TAC ATT TAG 2218

Fig. 24D

ACTGGTGAGAAAGAGCAGCCAGGGGGTCAGGCTTTCAGTCACCACCCTCCTGCTGCCACAGAAGGAAGTTCTCAGTATA 2297

CACCACAGTGCACGTGCATGATGGAGCTGTGGGACCCTCTCTGGGCTGGGTCTCATCTGTAAGCTGCTACAGCCCAGAT 2376

GAACTCTGCCAGCCGCCAGTGCATCCAGTACAGCGCCTGCCATCTTGTGCAATGTGCAACCCTGGGATGTGAGCCCTGC 2455

CATGTGCTGGTAACATGGCTAGGCATGTTGGGCTTCCCAAACCATGGAGTCTGGTAACCAGTGAAGGAAGCCCCCAGAA 2534

ATAATGAGTGGGGAAGGTACTAGGGCACTGGCCTTGGCCTCAAAAGTGCAGGCACACTTGAAACTGGAAAGGAAGGTGC 2613

TCTGGGCACATGTGGATTTGCTTCTATTGTTTTGTTTTGTTTTTTCTAATGTATTTATAAAAGATCTTTTCCCATTTAT 2692

GCTGGGAAAGTGTTTTTCAAACTCAGTGACAAGGACTTTGGTTTTTGTAAGACTGTTGATGATATGAAGGCCTTTTGTA 2771

AGAAAATAAAAAATAAAGTAAAAAAAAAAAAAAAAAAGGCGGCCGC 2815

Fig. 24E

```
                10        20        30        40        50
inputs MCSRVPLL-LPLLLLLALGPGVQGCPSGCQCSQPQTVFCTARQGTTVPRDVPPDTVGLYV
       : ::  :  : ::::. ::.:::::::::::.:::::::::::::::::::::::::::.
       MHSRSCLPPLLLLLLVLLGSGVQGCPSGCQCNQPQTVFCTARQGTTVPRDVPPDTVGLYI
               10        20        30        40        50        60

      60        70        80        90       100       110
inputs FENGITMLDAGSFAGLPGLQLLDLSQNQIASLPSGVFQPLANLSNLDLTANRLHEITNET
       :::::: ::.: :::::::::::::::::.:::.:.::::.::::::::::.::::.:::
       FENGITTLDVGCFAGLPGLQLLDLSQNQITSLPGGIFQPLVNLSNLDLTANKLHEISNET
               70        80        90       100       110       120

     120       130       140       150       160       170
inputs FRGLRRLERLYLGKNRIRHIQPGAFDTLDRLLELKLQDNELRALPPLRLPRLLLLDLSHN
       ::::::::::::::::::::::::::.:::::::::.:::::.::::.::::::::::::
       FRGLRRLERLYLGKNRIRHIQPGAFDALDRLLELKLPDNELRVLPPLHLPRLLLLDLSHN
              130       140       150       160       170       180

     180       190       200       210       220       230
inputs SLLALEPGILDTANVEALRLAGLGLQQLDEGLFSRLRNLHDLDVSDNQLERVPPVIRGLR
       :. :::.::::::::::::::::::.:::::::.:: :::::::::::::..:.::.:::
       SIPALEAGILDTANVEALRLAGLGLRQLDEGLFGRLLNLHDLDVSDNQLEHMPSVIQGLR
              190       200       210       220       230       240

     240       250       260       270       280       290
inputs GLTRLRLAGNTRIAQLRPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLRLLAAARNP
       :::::::::::::::.::::::::.::::::::::::::::.:::.::::::::::::::
       GLTRLRLAGNTRIAQIRPEDLAGLTALQELDVSNLSLQALPSDLSSLFPRLRLLAAARNP
              250       260       270       280       290       300
```

Fig. 25A

```
          300       310       320       330       340       350
inputs FNCVCPLSWFGPWVRESHVTLASPEETRCHFPPKNAGRLLLELDYADFGCPATTTTATVP
       :::.::::::::::::.::.:::::::::::::::::::::.:::::::::.::::::::
       FNCLCPLSWFGPWVRENHVVLASPEETRCHFPPKNAGRLLLDLDYADFGCPVTTTTATVP
                 310       320       330       340       350       360

          360       370       380       390       400       410
inputs TTRPVVREPTALSSSLAPTWLSPTAPATEAPSPPSTAPPTVGPVPQPQDCPPSTCLNGGT
       :.:...::::  .:: :::: : :.:.:.:..  ::::::. :.:::::::.:.:::::.
       TIRSTIREPTLSTSSQAPTWPSLTEPTTQASTVLSTAPPTMRPAPQPQDCPASICLNGGS
                 370       380       390       400       410       420

          420       430       440       450       460       470
inputs CHLGTRHHLACLCPEGFTGLYCESQMGQGTRPSPTPVTPRPPRSLTLGIEPVSPTSLRVG
       :.::.::: .:::::::.::::::.. :: .::..: :::::  : :.:::::::::::
       CRLGARHHWECLCPEGFIGLYCESPVEQGMKPSSIPDTPRPPPLLPLSIEPVSPTSLRVK
                 430       440       450       460       470       480

          480       490       500       510       520       530
inputs LQRYLQGSSVQLRSLRLTYRNLSGPDKRLVTLRLPASLAEYTVTQLRPNATYSVCVMPLG
       :::::::..:::::::::::::::::::::::::::::::::::::::::::::.:: :::
       LQRYLQGNTVQLRSLRLTYRNLSGPDKRLVTLRLPASLAEYTVTQLRPNATYSICVTPLG
                 490       500       510       520       530       540

          540       550       560       570       580       590
inputs PGRVPEGEEACGEAHTPPAVHSNHAPVTQAREGNLPLLIAPALAAVLLAALAAVGAAYCV
       .::.::::::::::.:..::.::::::::::::::::::::::::::::.:::.::::::
       AGRTPEGEEACGEANTSQAVRSNHAPVTQAREGNLPLLIAPALAAVLLAVLAAAGAAYCV
                 550       560       570       580       590       600
```

Fig. 25B

```
     600       610       620       630       640       650
inputs RRGRAMAAAAQDKGQVGPGAGPLELEGVKVPLEPGPKATEGGGEALPSGSECEVPLMGFP
       ::.:: ...::::::::.:::::::::.::::::.::::::::::..:.::::::::.:
       RRARA-TSTAQDKGQVGPGTGPLELEGVKAPLEPGSKATEGGGEALSGGPECEVPLMGYP
                610       620       630       640       650

     660       670
inputs GPGLQSPLHAKPYI
       ::.::. : :: ::
       GPSLQGVLPAKHYI
     660       670
```

Fig. 25C

```
                    1                                                          60
human LRSG-1        MCSR---VPLLLPLLLLLALGP-GVQG-------------CPSGCQCS-----QPQTVFC
murine LRSG-1       MHSRSC-LPPLL-LLLLVLLGS-GVQG-------------CPSGCQCN-----QPQTVFC
GPV                 N-LRGTLLCAVLGLLR-------------------AQPFPCPPACKCVFRDAAQ-----C
IGFBP               MALRKGGLALALLLLSWVALGPRSLEGAEPGTPGEAEGPACPATCACSYDDEVNELSVFC

                    61                                                        120
human LRSG-1        TARQGTTVPR-DVPPDTVGLYVFENGITMLDAGSFAGLPGLQLLDLSQNQIASLPSGVFQ
murine LRSG-1       TARQGTTVPR-DVPPDTVGLYIFENGITTLDVGCFAGLPGLQLLDLSQNQITSLPGGIFQ
GPV                 SGGDVARISALGLP-----------------------TNLTHILLFGMGRGVLQSQSFS
IGFBP               SSRNLTRLPD-GIPGGTQALWLDSNNLSSIPPAAFRNLSSLAFLNLQGGQLGSLEPQALL

                    121                                                       180
human LRSG- 1       PLANLSNLDLTANRLHEITNETFRGLRRLERLYLGKNRIRHIQPGAFDTLDRLLELKLQD
murine LRSG-1       PLVNLSNLDLTANKLHEISNETFRGLRRLERLYLGKNRIRHIQPGAFDALDRLLELKLPD
GPV                 GMTVLQRLMISDSHISAVAPGTFSDLIKLKTLRLSRNKITHLPGALLDKMVLLEQLFLDH
IGFBP               GLENLCHLHLERNQLRSLAVGTFAYTPALALLGLSNNRLSRLEDGLFEGLGNLWDLNLGW

                    181                                                       240
human LRSG-1        NELRALPPLRLPRLLLLD---LSHNSLLALEPGILDT-ANVEALRLAGLGLQQLDEGLFS
murine LRSG-1       NELRVLPPLHLPRLLLLD---LSHNSIPALEAGILDT-ANVEALRLAGLGLRQLDEGLFG
GPV                 NALRGIDQNMFQKLVNLQELALNQNQLDFLPASLFTNLENLKLLDLSGNNLTHLPKGLLG
IGFBP               NSLAVLPDAAFRGLGGLRELVLAGNRLAYLQPALFSGLAELRELDLSRNALRAIKANVFA

                    241                                                       300
human LRSG-1        RLRNLHDLDVSDNQLERV-PPVIRGLRGLTRLRLAGNTRIAQLRPEDLAGLAALQELDVS
murine LRSG-1       RLLNLHDLDVSDNQLEHM-PSVIQGLRGLTRLRLAGNTRIAQIRPEDLAGLTALQELDVS
GPV                 AQAKLERLLLHSNRLVSLDSGLLNSLGALTELQFH-RNHIRSIAPGAFDRLPNLSSLTLS
IGFBP               QLPRLQKLYLDRNLIAAVAPGAFLGLKALRWLDLS-HNRVAGLLEDTFPGLLGLRVLRLS
```

Fig. 26A

	301 360
human LRSG-1	*NLSLQALPGDLSGLFPRLRLLAAARNPFNCVCPLSWF*GPWVRESHVTLASPEETRCHFPP
murine LRSG-1	*NLSLQALPSDLSSLFPRLRLLAAARNPFNCLCPLSWF*GPWVRENHVVLASPEETRCHFPP
GPV	*RNHLAFLPSALFLHSHNLTLLTLFENPLAEL-PGVLFGEMGGLQELWLNRTQ--------*
IGFBP	*HNAIASLRPRTFEDLHFLEELQLGHNRIRQL-AERSFEGLGQLEVLTLDHNQ--------*
	361 420
human LRSG-1	KNAGRLLLELDYADFGCPATTTTATVPTTRPVVREPTALSSSLAPTWLSPTAPATEAPSP
murine LRSG-1	KNAGRLLLDLDYADFGCPVTTTTATVPTIRSTIREPTLSTSSQAPTWPSLTEPTTQASTV
GPV	*------L------------------------RT--------------LPAAAFRNLSR*
IGFBP	*------LQEVKVGAF--LGLTNVAVMNLSGNCLRN--------------LPEQVFRGLGK*
	421 * * * * * * 480
human LRSG-1	PSTAPPTVGPVPQPQDCPPSTCLNGGTCHLGTRHHLACLCPEGFTGLYCESQMGQGTRPS
murine LRSG-1	LSTAPPTMRPAPQPQDCPASICLNGGSCRLGARHHWECLCPEGFIGLYCESPVEQGMKPS
GPV	*LRYLGVTLSP------------------RLSA------LPQGAFQGL-------------*
IGFBP	*LHSLHLE-GS------------------CLGR------IRPHTFAGL-------------*
	481 540
human LRSG-1	PTPVTPR**PPRSLTLGIEPVSPTSLRVGLQRYLQGS--SVQLRSL-RLTYRNLSGPDKRLV**
murine LRSG-1	SIPDTPR**PPPLLPLSIEPVSPTSLRVKLQRYLQGN--TVQLRSL-RLTYRNLSGPDKRLV**
GPV	*---GELQVLALHSNGLTALPDGLLR-GLGKLRQVSLRRNRLRALPRALFRNLSSLESVQL*
IGFBP	*---SGLRRLFLKDNGLVGIEEQSLW-GLAELLELDLTSNQLTHLPHQLFQGLGKLEYLLL*
	541 600
human LRSG-1	**TLRLPASLAEYTVTQLRPNATYSVCV**MPLGPGRVPEGEEACGEAHTPPAVHSNHAPVTQA
murine LRSG-1	**TLRLPASLAEYTVTQLRPNATYSICV**TPLGAGRTPEGEEACGEANTSQAVRSNHAPVTQA
GPV	*DHNQLETLPGDVFGALPRLTEVLLGHNSW--------RCDCG-LGPFLGWLRQHLGL---*
IGFBP	*SHNRLAELPADALGPLQRAFWLDVSHNRL--------EALPGSLLASLGRLR-YLNL---*

Fig. 26B

	601	660
human LRSG-1	REGNLPLLIAPALAAVLLAALAAVGAAY-CVRRGRAMAAAAQDKGQVGPGAGPLELEGVK	
murine LRSG-1	REGNLPLLIAPALAAVLLAVLAAAGAAY-CVRRARA-TSTAQDKGQVGPGTGPLELEGVK	
GPV	VGGEEPPRCAGPGAHAGLPLWALPGGDAECPGPRGPPPRPAADSSSEAP---------VH	
IGFBP	*R--NNSLRTFTPQPPGLERLN-LEGNP*WDCSCPLKALRDFALQNPSAVP---------R-	
	661	720
human LRSG-1	VPLEPGPKATEGGGEALPSGS-ECEVPLMGF-----PGPGLQSP---------------L	
murine LRSG-1	APLEPGSKATEGGGEALSGGP-ECEVPLMGY-----PGPSLQGV---------------L	
GPV	PALAPNSSEPWVWAQPVTTGKGQDHSPFWGFYFLLLAVQAMITVIIVFAMIKIGQLFRKL	
IGFBP	------------FVQAICEG-DDCQPPVYTYNNITCASPPEVAGLDL----------RDL	
	721 728	
human LRSG-1	HAKPYI--	
murine LRSG-1	PAKHYI--	
GPV	IRER-ALG	
IGFBP	GEAHFAPC	

Fig. 26C

GAATTCCCGGGTCGACCCACGCGTCCGCCCACGCGTCCGCCCACGCGTCCGGCTGAGCGAAGCGCGGCGGCGGCGG 79

CGCCTAGGGGAGGGAGGGGCGGCGGGGCCGAGCCCACCTAGCGGAGCGCGCCGGCCGCCGGTGGCCGCCGCCAGCATGC 158

CCCGGCCCGCGGGCCGCTCCGCCGCCAGCCACCCCCGCGGCCCTCGGCGGCCTGCGCTCGGCCCGGGGGCGCGGAACC 237

GCAGCCGGAGCCGGAGGCGGGAGCAGCGAGCCGGAGCCCCGGGCGCTCGAATGCAGGATGCTCGTGGTCCCCAGCATCC 316

TTGAGCCACCAGGAGTGAGGGCTGCTGCTCCCTGAGACCTGGCTCCAAGGAGGATGCCACAGCCGCCTGCCAGCTCCGG 395

M S D E R R L P G S A V G W L V C 17

TCTGCACC ATG AGT GAT GAG CGG CGG CTG CCT GGC AGT GCA GTG GGC TGG CTG GTA TGT 454

G G L S L L A N A W G I L S V G A K Q K 37

GGG GGC CTC TCC CTG CTG GCC AAT GCC TGG GGC ATC CTC AGC GTT GGC GCC AAG CAG AAG 514

K W K P L E F L L C T L A A T H M L N V 57

AAG TGG AAG CCC TTG GAG TTC CTG CTG TGT ACG CTC GCG GCC ACC CAC ATG CTA AAT GTG 574

A V P I A T Y S V V Q L R R Q R P D F E 77

GCC GTG CCC ATC GCC ACC TAC TCC GTG GTG CAG CTG CGG CGG CAG CGC CCC GAC TTC GAG 634

W N E G L C K V F V S T F Y T L T L A T 97

TGG AAT GAG GGT CTC TGC AAG GTC TTC GTG TCC ACC TTC TAC ACC CTC ACC CTG GCC ACC 694

C F S V T S L S Y H R M W M V C W P V N 117

TGT TTC TCT GTC ACC TCC CTC TCC TAC CAC CGC ATG TGG ATG GTC TGC TGG CCT GTC AAC 754

Y R L S N A K K Q A V H T V M G I W M V 137

TAC CGG CTG AGC AAT GCC AAG AAG CAG GCG GTG CAC ACA GTC ATG GGT ATC TGG ATG GTG 814

S F I L S A L P A V G W H D T S E R F Y 157

TCC TTC ATC CTG TCG GCC CTG CCT GCC GTT GGC TGG CAC GAC ACC AGC GAG CGC TTC TAC 874

T H G C R F I V A E I G L G F G V C F L 177

ACC CAT GGC TGC CGC TTC ATC GTG GCT GAG ATC GGC CTG GGC TTT GGC GTC TGC TTC CTG 934

L L V G G S V A M G V I C T A I A L F Q 197

CTG CTG GTG GGC GGC AGC GTG GCC ATG GGC GTG ATC TGC ACA GCC ATC GCC CTC TTC CAG 994

T L A V Q V G R Q A D H R A F T V P T I 217

ACG CTG GCC GTG CAG GTG GGG CGC CAG GCC GAC CAC CGC GCC TTC ACC GTG CCC ACC ATC 1054

V V E D A Q G K R R S S I D G S E P A K 237

GTG GTG GAG GAC GCG CAG GGC AAG CGG CGC TCC TCC ATC GAT GGC TCG GAG CCC GCC AAA 1114

T S L Q T T G L V T T I V F I Y D C L M 257

ACC TCT CTG CAG ACC ACG GGC CTC GTG ACC ACC ATA GTC TTC ATC TAC GAC TGC CTC ATG 1174

G F P V L D S T P I P E R S A V R Q G E 277

GGC TTC CCT GTG CTG GAC TCT ACG CCC ATC CCC GAA AGG TCT GCA GTG AGA CAG GGA GAG 1234

D W G K D Q P E G F H P S S R Q D C L P 297

GAC TGG GGC AAA GAC CAG CCT GAG GGG TTT CAT CCA AGC AGC AGG CAA GAC TGC CTT CCC 1294

* 298

TGA 1297

Fig. 27A

GCCATTGCAGGACATGAGGACATGAGCTCCAGAATGGTGCCAGGCCGAGCCCTGTGCCCACAGGTGGTGAGCTTCAGCA 1376

GCCTGCGGGCCGACGCCTCAGCGCCCTGGATGGCACTCTGCGTGCTGTGGTGCTCCGTGGCCCAGGCCCTGCTTCCGAC 1455

CTGTCCTGCCTCAGTTTCCCCATCTGTGATGAGCAGGTGACCACGTTAACTCTCAGGGCTGTTTGAAGTCTCTTGGTTG 1534

TAGGCCCTCGCCACTGAGTGGCCCAGGTGTGAGAGGTAGTCTAGAGCCCTCTGCGGCCTTTGTGGAGGTCCGTTCTCAG 1613

CATGTGGCCTGGTGTGGCTCCCTAGGCCTGAGGCCTCCCACTCTCAGTGCCCCCTGCCCCCTTGGGAACCCACACTCCA 1692

CCCCAGCTAAGCACAACACTGTGGACCACCACCAATGGCACCTGAGCCACCTTGACCACCATTAGTGTCCCCACCCTCA 1771

TTACTCTGCCGTCGTTGCCTGTCCCCACCACATCATCTCCCTCCATGGCTCCCACCATGACGCTGGCAGGTGCAAGCGG 1850

AGAGCACGAGGGCAGCAGGGCCTGGCCTTCCGTGTCCCTGCGTCATCCCCAGCCTCACTCCCCACCCGTGCAGGCCTGG 1929

CCAGGAAGGGATCCTGGCAGGGGCTTCCAGGTTCTCAGCTCAAGGCCTGGTCCCGGGCAGGCGTCCAACCCCTGGGAGC 2008

AATGTATTTCTTTGCCTTCCATCCTGGGCAGACCCCTTACAGGCCTGGGCATTGCCATGGGCCCTGGGTCTTCCCAGGC 2087

TAAGGAGAACCAGGAACAGCTATAACCTTGAGCTAGTGAAATAGGGTAGATGAGAAGGCTGTCTCCTCCAGACCCCTAC 2166

CCCTACACAGTGGCCCCACAATATGAAGACCTGGGGTAATTCCAAGGTGAGCATAGAGCCTGCCTGTGCCCAGTTCCTT 2245

CTGGCCCTCAGGTGGCCAAGCCCATCTCTTCATCCTTCAGATAGGGTCCCACTCCCAGAAGAAGCTGCTGGGGTGGGGG 2324

TGGGAGGCTGCCTAAGCCTGTCTGTGCTTCAGAGGCCCCTCCAGTCCCTGGCTGTGGGGTAACTGGGGGTATGAGCTGT 2403

GGCCACAGGTGAGCAAGGCAGGGAACTGCAATCCAGCCCTGGCCGCGGGAGGGGCCATCTCTGGCCAATGCTGCTGTGC 2482

CTTCAAGGACTGACAAGTTACGTAGGGGCAGAGGTCGCCAGCTAGCCAGTGTCTCCTCCATCTGGGGGGCGTCTGTCCA 2561

CTTGTCACCTTAGGTTTTCACTCATTTGTCACCTTGGGGTTTTGCTCTGTGTGTTTCATATCCAACGGCAATACTTGCA 2640

GGGGGACAGAGTCCTCTAAATACTCCAATCCTGCGGTTTTTACAAACATAAAGGGGGAGACCCCAAGTGGAGGACCCTG 2719

GGCCTGGAGCTCCCTCCCAAACTTTGTCCAGCATCCAGCCTGTTCCCTGGCTCACTGGGGAGGGAGTTGTCTTCATAG 2798

CACACCCAGAGCCAGGGATCCCTTTGTAGTTTTTTGACAACGGAGCATTTCTCTTCTGTACAGGACCCAATAAAAACTT 2877

CCTTATGATTTGCAAAAAAAAAAAAAAAGGGCGGCCGC 2915

Fig. 27B

GAATTCCCGGGTCGACCCACGCGTCCGGCGGCGGGGCCGAGCCCACCTAGCGGAGCGCGCCGGCCGCCGGTGGCCGCCG 79

CCAGCATGCCCCGGCCCGCGGGCCGCTCCGCCGCCAGCCACCCCCGCGGCCCTCGGCGGCCTGCGCTCGGCCCGGGGGC 158

GCGGGAACCGCAGCCGGAGCCGGAGGCGGGAGCAGCGAGCCGGAGCCCCGGGCGCTCGAATGCAGGATGCTCGTGGTCC 237

CCAGCATCCTTGAGCCACCAGGAGTGAGGGCTGCTGCTCCCTGAGACCTGGCTCCAAGGAGGATGCCACAGCCGCCTGC 316

M S D E R R L P G S A V G W L 15
CAGCTCCGGTCTGCACC ATG AGT GAT GAG CGG CGG CTG CCT GGC AGT GCA GTG GGC TGG CTG 378

V C G G L S L L A N A W G I L S V G A K 35
GTA TGT GGG GGC CTC TCC CTG CTG GCC AAT GCC TGG GGC ATC CTC AGC GTT GGC GCC AAG 438

Q K K W K P L E F L L C T L A A T H M L 55
CAG AAG AAG TGG AAG CCC TTG GAG TTC CTG CTG TGT ACG CTC GCG GCC ACC CAC ATG CTA 498

N V A V P I A T Y S V V Q L R R Q R P D 75
AAT GTG GCC GTG CCC ATC GCC ACC TAC TCC GTG GTG CAG CTG CGG CGG CAG CGC CCC GAC 558

F E W N E G L C K V F V S T F Y T L T L 95
TTC GAG TGG AAT GAG GGT CTC TGC AAG GTC TTC GTG TCC ACC TTC TAC ACC CTC ACC CTG 618

A T C F S V T S L S Y H R M W M V C W P 115
GCC ACC TGT TTC TCT GTC ACC TCC CTC TCC TAC CAC CGC ATG TGG ATG GTC TGC TGG CCT 678

V N Y R L S N A K K Q A V H T V M G I W 135
GTC AAC TAC CGG CTG AGC AAT GCC AAG AAG CAG GCG GTG CAC ACA GTC ATG GGT ATC TGG 738

M V S F I L S A L P A V G W H D T S E R 155
ATG GTG TCC TTC ATC CTG TCG GCC CTG CCT GCC GTT GGC TGG CAC GAC ACC AGC GAG CGC 798

F Y T H G C R F I V A E I G L G F G V C 175
TTC TAC ACC CAT GGC TGC CGC TTC ATC GTG GCT GAG ATC GGC CTG GGC TTT GGC GTC TGC 858

F L L L V G G S V A M G V I C T A I A L 195
TTC CTG CTG CTG GTG GGC GGC AGC GTG GCC ATG GGC GTG ATC TGC ACA GCC ATC GCC CTC 918

F Q T L A V Q V G R Q A D H R A F T V P 215
TTC CAG ACG CTG GCC GTG CAG GTG GGG CGC CAG GCC GAC CAC CGC GCC TTC ACC GTG CCC 978

T I V V E D A Q G K R R S S I D G S E P 235
ACC ATC GTG GTG GAG GAC GCG CAG GGC AAG CGG CGC TCC TCC ATC GAT GGC TCG GAG CCC 1038

A K T S L Q T T G L V T T I V F I Y D C 255
GCC AAA ACC TCT CTG CAG ACC ACG GGC CTC GTG ACC ACC ATA GTC TTC ATC TAC GAC TGC 1098

L M G F P V L V V S F S S L R A D A S A 275
CTC ATG GGC TTC CCT GTG CTG GTG GTG AGC TTC AGC AGC CTG CGG GCC GAC GCC TCA GCG 1158

P W M A L C V L W C S V A Q A L L L P V 295
CCC TGG ATG GCA CTC TGC GTG CTG TGG TGC TCC GTG GCC CAG GCC CTG CTG CTG CCT GTG 1218

F L W A C D R Y R A D L K A V R E K C M 315
TTC CTC TGG GCC TGC GAC CGC TAC CGG GCT GAC CTC AAA GCT GTC CGG GAG AAG TGC ATG 1278

A L M A N D E E S D D E T S L E G G I S 335
GCC CTC ATG GCC AAC GAC GAG GAG TCA GAC GAT GAG ACC AGC CTG GAA GGT GGC ATC TCC 1338

Fig. 28A

```
 P   D   L   V   L   E   R   S   L   D   Y   G   Y   G   G   D   F   V   A   L    355
CCG GAC CTG GTG TTG GAG CGC TCC CTG GAC TAT GGC TAT GGA GGT GAT TTT GTG GCC CTA  1398

 D   R   M   A   K   Y   E   I   S   A   L   E   G   G   L   P   Q   L   Y   P    375
GAT AGG ATG GCC AAG TAT GAG ATC TCC GCC CTG GAG GGG GGC CTG CCC CAG CTC TAC CCA  1458

 L   R   P   L   Q   E   D   K   M   Q   Y   L   Q   V   P   P   T   R   R   F    395
CTG CGG CCC TTG CAG GAG GAC AAG ATG CAA TAC CTG CAG GTC CCG CCC ACG CGG CGC TTC  1518

 S   H   D   D   A   D   V   W   A   A   V   P   L   P   A   F   L   P   R   W    415
TCC CAC GAC GAT GCG GAC GTG TGG GCC GCC GTC CCG CTG CCC GCC TTC CTG CCG CGC TGG  1578

 G   S   G   E   D   L   A   A   L   A   H   L   V   L   P   A   G   P   E   R    435
GGC TCC GGC GAG GAC CTG GCC GCC CTG GCG CAC CTG GTG CTG CCT GCC GGG CCC GAG CGG  1638

 R   R   A   S   L   L   A   F   A   E   D   A   P   P   S   R   A   R   R   R    455
CGC CGC GCC AGC CTC CTG GCC TTC GCG GAG GAC GCA CCA CCG TCC CGC GCG CGC CGC CGC  1698

 S   A   E   S   L   L   S   L   R   T   S   A   L   D   S   G   P   R   G   A    475
TCG GCC GAG AGC CTG CTG TCG CTG CGG ACC TCG GCC CTG GAT AGC GGC CCG CGG GGA GCC  1758

 R   D   S   P   P   G   S   P   R   R   R   P   G   P   G   P   R   S   A   S    495
CGC GAC TCG CCC CCC GGC AGC CCG CGC CGC CGC CCC GGG CCC GGC CCC CGC TCC GCC TCG  1818

 A   S   L   L   P   D   A   F   A   L   T   A   F   E   C   E   P   Q   A   L    515
GCC TCG CTG CTG CCC GAC GCC TTC GCC CTG ACC GCC TTC GAG TGC GAG CCA CAG GCC CTG  1878

 R   R   P   P   G   P   F   P   A   A   P   A   A   P   D   G   A   D   P   G    535
CGC CGC CCG CCC GGG CCC TTC CCC GCT GCG CCC GCC GCC CCC GAC GGC GCA GAT CCC GGA  1938

 E   A   P   T   P   P   S   S   A   Q   R   S   P   G   P   R   P   S   A   H    555
GAG GCC CCG ACG CCC CCA AGC AGC GCC CAG CGG AGC CCA GGG CCA CGC CCC TCT GCG CAC  1998

 S   H   A   G   S   L   R   P   G   L   S   A   S   W   G   E   P   G   G   L    575
TCG CAC GCC GGC TCT CTG CGC CCC GGC CTG AGC GCG TCG TGG GGC GAG CCC GGG GGG CTG  2058

 R   A   A   G   G   G   G   S   T   S   S   F   L   S   S   P   S   E   S   S    595
CGC GCG GCG GGC GGC GGC GGC AGC ACC AGC AGC TTC CTG AGT TCC CCC TCC GAG TCC TCG  2118

 G   Y   A   T   L   H   S   D   S   L   G   S   A   S   *                        610
GGC TAC GCC ACG CTG CAC TCG GAC TCG CTG GGC TCC GCG TCC TAG                      2163

GACCGCCGGCGCCTCCCCACGGACGCCAGGCAGGCCAGGCCGCTCTCCGGGGCCGCAGCACCAAAGACGCCCGCCTCCC  2242

CCCCGCGCGCAGACATGCGCCACCCCTCCCAGGGGTGAGGGGGCGTTGGCCTCAGCGTTTGTCTTCCGGCTCCTCCCAG  2321

CTGGCCTTGTCCCAGGGGCGACGGCTGCCCCGGACGACTGCGCTGGGCACCGCATGTCCCGGGCCGAGTGAGGTCGGGC  2400

CTGGGGAGCTGAGTGACATCCCAAGCTTGGGCTTGGGTAGTGAGTGACATGTGCACACGTCCAGCTGCGCCATCACCAG  2479

CCCTGCGCAACAGGACGTCGGGAGCAGGGAACCTGAGACAGGGCCACTGCGGGATCGGACAAAGCCCCGCTTTGGAGAG  2558

GCTGAGCTGGAGCCATTGGCCTCCCCAGGGGCTTTCCACCCACACTGCACCATAACCGCCACACCCTTCGGGGGGGGG  2637

AGGGTACAGAGGGTCTCTAAGCACAGGGGTGTTCAGAGCCCGAACAAGCTTTGATCAGGTTTCCCTGCTTCCGACCTGT  2716

CCTGCCTCAGTTTCCCCATCTGTGATGAGCAGGTGACCACGTTAACTCTCAGGGCTGTTTGAAGTCTCTTGGTTGTAGG  2795
```

Fig. 28B

CCCTCGCCACTGAGTGGCCCAGGTGTGAGAGGTAGTCTAGAGCCCTCTGCGGCCTTTGTGGAGGTCCGTTCTCAGCATG 2874

TGGCCTGGTGTGGCTCCCTAGGCCTGAGGCCTCCCACTCTCAGTGCCCCCTGCCCCCTTGGGAACCCACACTCCACCCC 2953

AGCTAAGCACAACACTGTGGACCACCACCAATGGCACCTGAGCCACCTTGACCACCATTAGTGTCCCCACCCTCATTAC 3032

TCTGCCGTCGTTGCCTGTCCCCACCACATCATCTCCCTCCATGGCTCCCACCATGACGCTGGCAGGTGCAAGCGGAGAG 3111

CACGAGGGCAGCAGGGCCTGGCCTTCCGTGTCCCTGCGTCATCCCCAGCCTCACTCCCCACCCGTGCAGGCCTGGCCAG 3190

GAAGGGATCCTGGCAGGGGCTTCCAGGTTCTCAGCTCAAGGCCTGGTCCCGGGCAGGCGTCCAACCCCTGGGAGCAATG 3269

TATTTCTTTGCCTTCCATCCTGGGCAGACCCCTTACAGGCCTGGGCATTGCCATGGGCCCTGGGTCTTCCCAGGCTAAG 3348

GAGAACCAGGAACAGCTATAACCTTGAGCTAGTGAAATAGGGTAGATGAGAAGGCTGTCTCCTCCAGACCCCTACCCCT 3427

ACACAGTGGCCCCACAATATGAAGACCTGGGGTAATTCCAAGGTGAGCATAGAGCCTGCCTGTGCCCAGTTCCTTCTGG 3506

CCCTCAGGTGGCCAAGCCCATCTCTTCATCCTTCAGATAGGGTCCCACTCCCAGAAGAAGCTGCTGGGGTGGGGGTGGG 3585

AGGCTGCCTAAGCCTGTCTGTGCTTCAGAGGCCCCTCCAGTCCCTGGCTGTGGGGTAACTGGGGGTATGAGCTGTGGCC 3664

ACAGGTGAGCAAGGCAGGGAACTGCAATCCAGCCCTGGCCGCGGGAGGGGCCATCTCTGGCCAATGCTGCTGTGCCTTC 3743

AAGGACTGACAAGTTACGTAGGGGCAGAGGTCGCCAGCTAGCCAGTGTCTCCTCCATCTGGGGGGCGTCTGTCCACTTG 3822

TCACCTTAGGTTTTCACTCATTTGTCACCTTGGGGTTTTGCTCTGTGTGTTTCATATCCAACGGCAATACTTGCAGGGG 3901

GACAGAGTCCTCTAAATACTCCAATCCTGCGGTTTTTACAAACATAAAGGGGGAGACCCCAAGTGGAGGACCCTGGGCC 3980

TGGAGCTCCCTCCCAAACTTTGTCCAGCATCCAGCCTGTTCCCTGGGCTCACTGGGGAGGGAGTTGTCTTCATAGCACA 4059

CCCAGAGCCAGGGATCCCTTTGTAGTTTTTTGACAACGGAGCATTTCTCTTCTGTACAGGACCCAATAAAAACTTCCTT 4138

ATGAAAAAAAAAAAAAAAGGGCGGCCGC 4166

Fig. 28C

```
            1                                                          60
SSTM-1      MS------DERRLPGSAVGWLVCGGLSLLANAWGILSVGAKQKKWKPLEFLLCTLAATHM
SSTM-2      MS------DERRLPGSAVGWLVCGGLSLLANAWGILSVGAKQKKWKPLEFLLCTLAATHM
proteinA-2  MARGGAGAEEASLRSNALSWLACGLLALLANAWIILSISAKQQKHKPLELLLCFLAGTHI
proteinA-3  ------------------------------------------------------------

            61                                                        120
SSTM-1      LNVAVPIATYSVVQLRRQ-RPDFEWNEGLCKVFVSTFYTLTLATCFSVTSLSYHRMWMVC
SSTM-2      LNVAVPIATYSVVQLRRQ-RPDFEWNEGLCKVFVSTFYTLTLATCFSVTSLSYHRMWMVC
proteinA-2  LMAAVPLTTFAVVQLRRQASSDYDWNESICKVFVSTYYTLALATCFTVASLSYHRMWMVR
proteinA-3  ------------------------------------------------------------

            121                                                       180
SSTM-1      WPVNYRLSNAKKQAVHTVMGIWMVSFILSALPAVGWHDTSERFYTHGCRFIVAEIGLGFG
SSTM-2      WPVNYRLSNAKKQAVHTVMGIWMVSFILSALPAVGWHDTSERFYTHGCRFIVAEIGLGFG
proteinA-2  WPVNYRLSNAKKQALHAVMGIWMVSFILSTLPSIGWHNNGERYYARGCQFIVSKIGLGFG
proteinA-3  ------------------------------------------------------------

            181                                                       240
SSTM-1      VCFLLLVGGSVAMGVICTAIALFQTL--------------------AVQVGRQADHRAFT
SSTM-2      VCFLLLVGGSVAMGVICTAIALFQTL--------------------AVQVGRQADHRAFT
proteinA-2  VCFSLLLLGGIVMGLVCVAITFYQTLWARPRRARQARRVGGGGGTKAGGPGALGTRPAFE
proteinA-3  -------------------ITFYQTLWARPRRARQARRVGGGGGTKAGGPGALGTRPAFE

            241                                                       300
SSTM-1      VPTIVVEDAQGKRRSSIDGSEPAKTSLQTTGLVTTIVFIYDCLMGFPVL-----------
SSTM-2      VPTIVVEDAQGKRRSSIDGSEPAKTSLQTTGLVTTIVFIYDCLMGFPVLVVSFSSLRADA
proteinA-2  VPAIVVEDARGKRRSSLDGSESAKTSLQVTNLVSAIVFLYDSLTGVPILVVSFFSLKSDS
proteinA-3  VPAIVVEDARGKRRSSLDGSESAKTSLQVTNLV-----------------VSFFSLKSDS

            301                                                       360
SSTM-1      ----------------------------------------------------DSTPI---
SSTM-2      SAPWMALCVLWCSVAQALLLPVFLWACDRYRADLKAVREKCMALMANDEESDDETSLEGG
proteinA-2  APPWMVLAVLWCSMAQTLLLPSFIWSCERYRADVRTVWEQCVAIMSEEDGDDD------G
proteinA-3  APPWMVLAVLWCSMAQTLLLPSFIWSCERYRADVRTVWEQCVAIMSEEDGDDD------G

            361                                                       420
SSTM-1      -----------------------------------------------------------P
SSTM-2      ISPDLVLER--SLDYGYGGDFVALDRMAKYEISALEGGLPQLYPLRPLQEDKMQYLQVPP
proteinA-2  GCDDYAEGRVCKVRFDANGATGPGSRDPA-QVKLLPGR-HMLFP--PL--ERVHYLQVPL
proteinA-3  GCDDYAEGRVCKVRFDANGATGPGSRDPA-QVKLLPGR-HMLFP--PL--ERVHYLQLK-

            421                                                       480
SSTM-1      ERSAVRQGED--------------WGKDQ-------------------------------
SSTM-2      TRRFSHDDADVWAAVPLPA-FLPRWGSGEDLAALAHLVLP-AGPERRRASLLAFAEDAPP
proteinA-2  SRRLSHDETNIFSTPREPGSFLHKWSSSDDIRVLPAQSRALGGPPEYLGQRHRLEDEEDE
proteinA-3  KLDLAAAAAHTF----------------------------------FVANPMHLQ-----

            481                                                       540
SSTM-1      --------------------------------------------------PEGFH-----
SSTM-2      SRARRRSAESLLSLRTSALDSGPRGARDSPPGSPRRRPGPGPRSASASLLPDAFALTAFE
proteinA-2  EEA---EGGGLASLRQF-LESGVLGSGGGPP------RGPG-------FFRE--EITTF-
proteinA-3  -------------------------------------------------MRE--DMAKY-
```

Fig. 29A

```
            541                                                          600
SSTM-1      ---------------------------------------PSSRQ-----------------
SSTM-2      CEPQALRRPPGPFPAAPAAPDGADPGEAPTPPSSAQRSPGPRP--SAHSHAGSLRPGLSA
proteinA-2  ------------IDETPLPSPTASPGHSPRRPRPLGLSPRRLSLGSPESRAVGLPLGLSA
proteinA-3  ----------------------------------------RRMS-----------------

            601                                      642
SSTM-1      ------------------------------------DCL---P
SSTM-2      SWGEPGGLRAAGGGGSTSSFLSSPSESSGYATLHSDSLGSAS
proteinA-2  ------GRRCSLTGGEESARAWGGSWGPGNPIFPQLTL----
proteinA-3  ------GVR---------------------------------
```

Fig. 29B

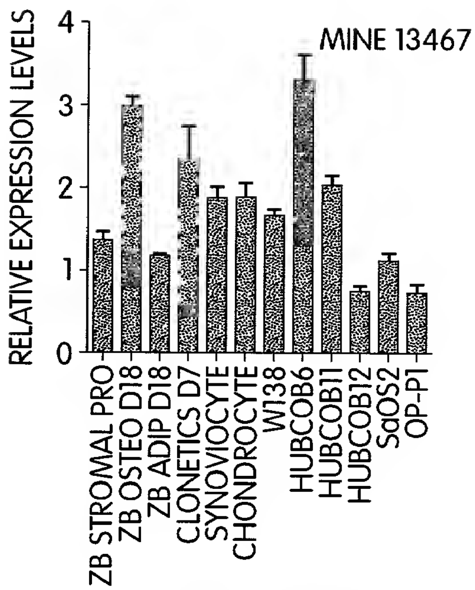

Fig. 30A

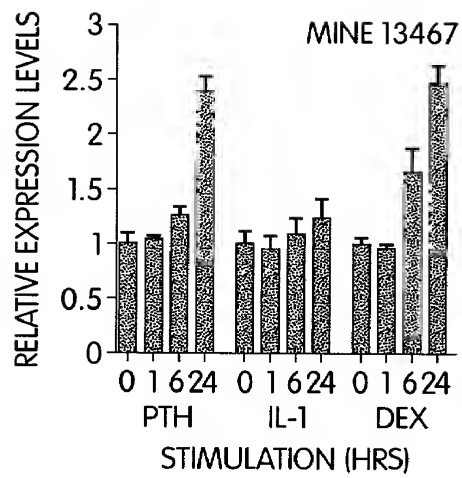

Fig. 30B

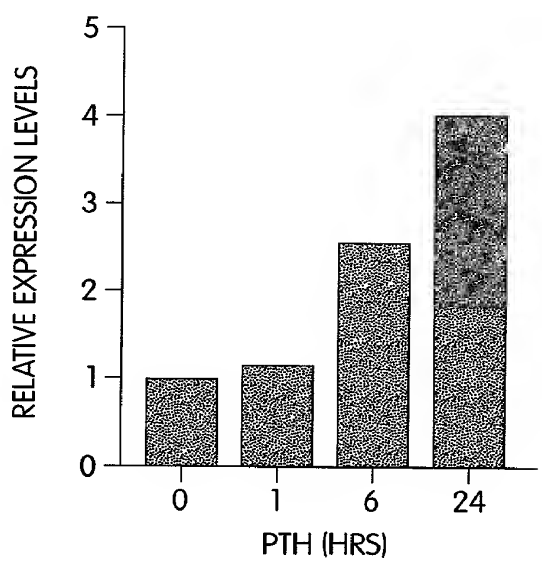

Fig. 30C

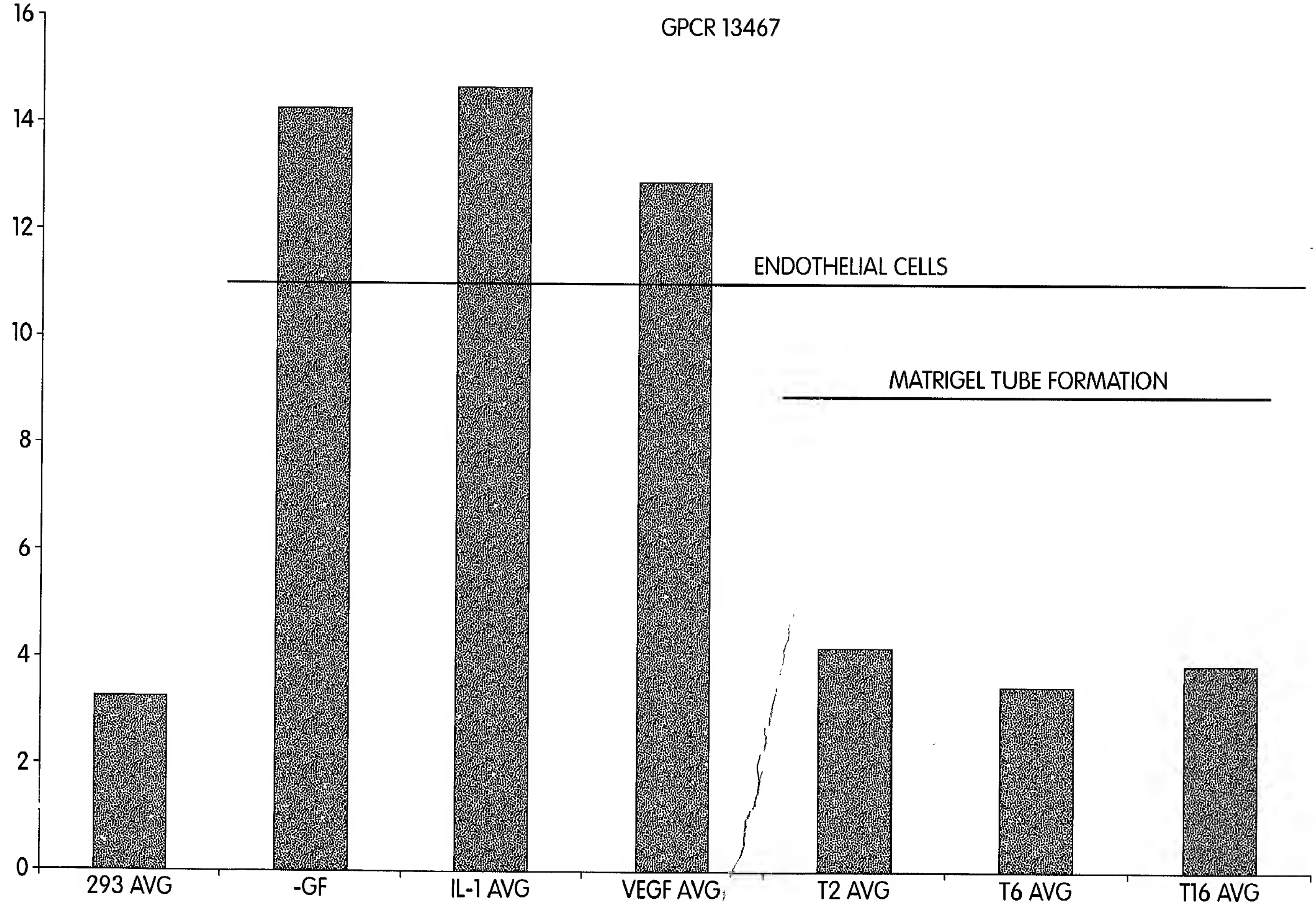
GPCR 13467
16
14
12
10
8
6
4
2
0
ENDOTHELIAL CELLS
MATRIGEL TUBE FORMATION
293 AVG
-GF
IL-1 AVG
VEGF AVG
T2 AVG
T6 AVG
T16 AVG

Fig. 31